

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:06:29 ; Search time 40 Seconds

(without alignments)
1255.629 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 1 MLRLVRLKRWPLEVPEPTE.....DRPPFRPSRGRTDGLSPM 522

Sequence: 1 MLRLVRLKRWPLEVPEPTE.....DRPPFRPSRGRTDGLSPM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 263416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 263416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR 791:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240.5	8.7	475	2 A86372	53.0K hypothetical
2	187.5	6.8	350	2 H86371	40.0K hypothetical
3	145.5	5.3	547	2 T46356	hypothetical prote
4	128.5	4.7	842	2 T32258	hypothetical prote
5	118	4.3	564	2 H70804	hypothetical prote
6	117.5	4.3	1213	2 A41724	limb deformity (ld
7	117	4.2	403	2 S52796	prpl2 protein - hu
8	116.5	4.2	915	2 T12586	hypothetical prote
9	115	4.2	4957	2 T03455	ALR protein - huma
10	115	4.2	5262	2 T03454	ALR protein - huma
11	112	4.1	1006	2 G86252	hypothetical prote
12	111.5	4.0	940	2 JEO251	FB19 protein - hum
13	111	4.0	1097	2 T49187	hypothetical prote
14	110.5	4.0	551	2 S57447	HPBR1-7 protein -
15	110	4.0	424	2 A54964	spliceosome-associ
16	110	4.0	1468	2 S11515	formin mouse
17	109.5	4.0	742	2 A49672	transcription fact
18	109.5	4.0	772	2 A55004	transcription fact
19	109	4.0	741	2 T46356	probable transcrip
20	109	4.0	1206	2 S24407	formin isoform IV
21	109	4.0	2783	1 A41948	alpha-fetoprotein
22	108	3.9	311	2 T15997	hypothetical prote
23	108	3.9	577	2 T09004	hypothetical prote
24	107.5	3.9	589	2 T29259	proline-rich prote
25	107	3.9	351	1 USB7P1	hypothetical prote
26	107	3.9	505	2 A53152	centromere-binding
27	107	3.9	1257	2 T01020	annexin XI - human
28	106.5	3.9	212	2 S57330	hypothetical prote
29	106.5	3.9	584	2 G71676	cathelin-like anti
					hypothetical prote

30	106	3.8	401	2 T51407	proline-rich prote
31	106	3.8	444	2 E83802	hypothetical prote
32	105.5	3.8	828	2 T06133	hypothetical prote
33	105.5	3.8	882	2 T43250	spindle pole body-
34	105.5	3.8	897	2 A39405	beta-galactosidase
35	105.5	3.8	1465	2 T23056	chromodomain helic
36	105	3.8	502	2 A55197	Wiskott-Aldrich sy
37	105	3.8	715	2 G86239	protein F20B24.6 l
38	104.5	3.8	235	2 A72594	hypothetical prote
39	104.5	3.8	301	2 J01663	hybrid proline-ric
40	104.5	3.8	850	2 J05047	ras GTPase-activat
41	104	3.8	178	2 T36013	probable integrat
42	104	3.8	188	2 D29149	proline-rich prote
43	104	3.8	574	2 H86467	probable transcrip
44	104	3.8	708	2 D96711	hypothetical prote
45	104	3.8	1252	2 D71810	probable type II D

ALIGNMENTS

RESULT 1

A86372
53.0K hypothetical protein F508.33 - Arabidopsis thalianaC:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004C:Accession: A86372
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,Chen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzalli,Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Iker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A86372

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-475 <STO>

A:Cross-references: UNIPROT:Q9ZUB8; GB:A8005172; NID:94056460; PIDN:AAC98033.1; GSPDB:GNL

C:Genetics:

A:Map position: 1

Query Match	Score	DB 2	Length
Best Local Similarity	24.5%	Pred. No. 1.2e-09;	475;
Matches	116;	Conservative	89; Mismatches 177; Indels 91; Gaps 20;
1	MLRLVRLKRWPLEVPEPTEPTLGLRSHRLSLCTGVSNNRFTTLNKKPL--TG	58	
3	LRRLHRETKLEFLAAD--TLHDLRRINPTV-----PSSVHSLNRKDELTPS	53	
59	DEETLASGVISGDIICLLLODDIPAPNIPSTSTSESHSSLNNEQPSIATSSNOTS	118	
54	PEDTIRSLGLISGDIYPSLE-----AGESNNKLDSEITVASQSNSQTSVHD	102	
119	QPSDSFGQAQSGYWNDSYMLGPSNFASIQNNAMAG--TGFPSPM-----	169	
103	--STGP-----AEVDVVPQAKSNPR-----TSVED-----PGSDISGMEGPPMDVEQJDM	147	
170	--LCSSEYGVQPHSLER--LYQADSCDANDALIVLHLMBSGY--PQGT-----	218	
148	ELAAAGSRKLSPEFLKNTLLKSGDSTELR--TLASVHAWLBSGFLNMGSDKFNFS	206	
219	AKALSMPEKMLSGYKQYHAPLCESSATILTCPLGNLVNATL-----KINNE--	271	
207	KELLTVSRYTLPELIKSKDVTI--ESVSVPONLPPVAVVGTGCGSGRVAMNDK	263	
272	RSVRLQILPSEFCKEKELGENVANIYKDLQKSLRFLKFDOLVYLLAFTRQALNLPV	330	
264	RRFVVIDLVMDTSTDS--EGSSSIYREVFMFRVYKDLIV--PLLGICDKKGLSP	320	

QY 331 GLVVLPLELKLRIIRLLDVRSVLSAVCDLFTASNDPLMRFLYIRDNDNTVAV--Q 388
 Db 321 CLMRPLELKLRIIRLLDVRSVLSAVCDLFTASNDPLMRFLYIRDNDNTVAV--Q 388
 QY 389 DTDWK-----ELYRRHIOKESPPGRFVMLPSTHTIPF 424
 Db 381 SYWKAFATRWKQKLAASDTFRWQNGORNRISGRGIRFPRRIIDPPF 433

RESULT 2

40.0K hypothetical protein F508.32 - Arabidopsis thaliana
 H86371
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: H86371
 R/Title: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Hansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: H86371
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-350 <STO>
 A/Cross-references: UNIPROT:Q9ZUB9; GB:A8005172; NID:94056459; PIDN:MAC98032.1; GSPDB:GN
 C/Genetics:
 A/Map position: 1

Query Match 6.8%; Score 187.5; DB 2; Length 350;
 Best Local Similarity 24.4%; Pred. No. 5.2e-06;
 Matches 90; Conservative 58; Mismatches 118; Indels 103; Gaps 17;
 QY 172 SEVEGVPHSLF-----TLYQADCDSPANDALIVLHLMLESGYI 213
 Db 22 NSGEGPVMQVELAAKSKRLSEPFLLKVLKESGDTSLT-ALALSVHAVVLESGFV 80
 QY 214 --PGTF-----AKALNPEKMKLSGVYKIQYHPLCEGSSATLTCVPLGNLVNATL- 265
 Db 81 LLHDSGDKFSFKLSLVSRLYLPFLITRDKNTV--BSVYRFQNTIPRLVVGFTLG 137
 QY 266 ---KINNEISVVKRLQLLPESFICKEL--GENVANIYKDLQKLSRLFKDQVYVLLA 318
 Db 138 GSCKRVH--MISLKSRLPYIDLVDTLKEKGGSSSVYKRVFMVMKXDELVIPL- 194
 QY 319 FTRQALNLPVFG-----LVVPLELKLRIIRLLDVRSVLSAVCDLFTASNDPLM 372
 Db 195 -----IGLCDKAGLESPPCLMLLPLELKLRIIRLLDVRSVLSAVCDLFTASNDPLM 249
 QY 373 RFLVLRDRDNTVQ--DTWKELY-----RKR--HIORKESPKGFVMLPSTHTIP 423
 Db 250 EHKLCEBKGLMKLITGSDVWKKKFASFRKRLDLARNPTRK----- 266
 QY 424 FYPNPLMRPPSSRLPFGIIGEXYDQFTLLPYVGPDISSILPGSGTSPQFPL----- 478
 Db 297 --SNRPFLLPPRR-----DRREFPDRG-----PSDFYFGRDIP 331
 QY 479 RPRDPVCP 487
 Db 332 RDRFGPRDP 340

RESULT 3

T46366
 Hypothetical protein DKFZp434C0118.1 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C/Accession: T46366
 R/Ottewill, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 Submitted to the Protein Sequence Database, January 2000
 A/Reference number: Z23031
 A/Accession: T46366
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-547 <AAA>
 A/Cross-references: UNIPROT:Q9NT57; EMBL:AF137520
 A/Experimental source: adult testis; clone DKFZp434C0118
 C/Genetics:
 A/Note: DKFZp434C0118.1

Query Match 5.3%; Score 145.5; DB 2; Length 547;
 Best Local Similarity 21.7%; Pred. No. 0.011;
 Matches 98; Conservative 61; Mismatches 123; Indels 169; Gaps 24;
 QY 105 SLATSSNOTSMODEPSPSFGQAAGSGVNMDSLWG-PSNFRFAESIQDNANHAEGGCF 163
 Db 72 SSAETGRSRHDDTHPS--GGRCGGTSPSSAGSPASMAAE--EDCH----- 119
 QY 164 YSEBMLCSSEVGVPHSLFTLYQADCDSPANDALIVLHLMLESGYIPOGTEAVK-L 222
 Db 120 -----SDTVR-----ADDEBENS-----PAETDLOQL 143
 QY 223 SMPKMKLSGVYKIQYHPLCEG--SSATLTCVPL--GNLIVNATLKINNE----- 270
 Db 144 QM-----FRQWMEFLAPGVSSNLENRPPRAAGSLQKTSADTKGQEQAKERA 194
 QY 271 ---IRSV-----KRLQLPE-----SPICKELGENVANIY-----KDLQ 302
 Db 195 RELFLKAAVEEONGALYAIKPYRRAMQVLDIEFKITYTSSPDGQVGNYSIEDNDSDS 254
 QY 303 KLSRL--FKDQVYVPLAFTQALNL--PDV---FGLVVLPLELKLRIIRL--LD 348
 Db 255 KQADLLSYFQQO-----LTFQESVYKLCQPLSSQIHISVLPMEVLMYIFRWVSSDLD 309
 QY 349 VASVSLSAVCRDLFTASNDPLMRFLYIRDNDNTVAV--Q 388
 Db 310 LRSLSQLSLVCGFYICARDEPRIMKLACKVWGRGCTLVPTYSRWMTLR-----P 362
 QY 408 KGRFVMLPSSST-----HTIPYPNLHRPPSSRLPFGIIGEXYDQ 450
 Db 363 RVRFDGVYISKTTIYRQEGSLDGFYRAMQVYEV--RYIRFPDGHV----- 408
 QY 451 RPTLPYVGDPISSILPGSGTSPQFPLRPR 481
 Db 409 -----WMLTPEEPQSIIVRLRTR 427

RESULT 4

T32258
 Hypothetical protein C24A1.3 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T32258
 R/Connelly, M.
 submitted to the EMBL Data Library, September 1997
 A/Description: The sequence of C. elegans cosmid C24A1.
 A/Reference number: Z21141
 A/Accession: T32258
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: DNA
 A/Residues: 1-842 <CON>
 A/Cross-references: UNIPROT:O17055; EMBL:AF024491; PIDN:AA870312.1; GSPDB:GN00021; CESP:
 A/Experimental source: strain Bristol N2; clone C24A1
 A/Genes: CESP:C24A1.3
 A/Map position: 3
 A/Introns: 43/2; 189/3; 234/1; 351/1; 511/3; 578/3; 594/2; 636/2; 675/3

Query Match 4.7%; Score 128.5; DB 2; Length 842;
 Best Local Similarity 20.3%; Pred. No. 0.35;

Matches 109; Conservative 79; Mismatches 197; Indels 151; Gaps 25;

QY 14 LEVETETPTIGHRLSHRLSLCTWGYSSNTRETTILNYDPLTQGBENTLASYIGYSGD 73
D 334 MKTPGVDPNYQGGDGHATHSACYGHRLVQYLE-----NGADQSLASAPFEGAL 386
QY 74 ICLLDIDIPAPNIPSSDTSEHSLQNNQOPSLATSSNOTMODEOPSPFOQAQSGV 133
D 387 ----RQAGBGTNRPSKVVAIMAINRSDTPSSNAGSNVSLDDQTPV-----I 433
QY 134 W----NDDSLGPSQNFASIODNAHMAEGTGYFSEPMLCSESYEGC----VHSHLE 184
D 434 WAYERGHDAIVALLKHYAARTVEGD-----VCSEYSSGESSYTPLPSPFG 478
QY 185 TL-----YQADCSGDANDALIVLHLMLTESGY---IPQTEAKALSMPEKMLSGYXQ 237
D 479 RLISLRDRAKDLQLRBALPAPPHLCIAETEPQESIGSGSGFK-----YKGT 526
QY 238 YMHPLCEGSSATLTCVPLGNLIVNATLKNINIRSVKRLQLLPESFICKKLGENVANI 297
D 527 YR-----GKLV-----AVKRYRAM--AFGCKSE---TDML 551
QY 298 YKDLQKLSRLFKQOLVYVPLAFTROALNLPDVGVLVLEL-----KLIRFLD 348
D 552 CREVSILSRLAHPNVV---AFVGTSLDPSQFALITEFVNGSLFRRENGEKKNRYMD 607
QY 349 ----VRSVLSLSAVCRDLFTASNDPLLMRFL-----YLRFDNTVRVQDD 391
D 608 PAFRLRLSLDVARGMRYLHESAAKPVYHRDLNHNILIHADGSRVADGSGSFVQGRD 667
QY 392 WKELLYRKRIHQKESPK-----GRFWMLBSSHTHTPTFYNPLHPRPSSRLPQGITG 446
D 668 -ENLTKQPGNLRWMAPEVFSQSGKYRKVDVFSAFVITW--ELHTLELPPSHLKPPAAAA 724
QY 447 E--YDQ--RPLTPYVGD-----ISLIPGGETPSQFPPLPRDPVCPPLPGPN 492
D 725 EMTYKRGRIPLP--NQTAPFAHILSLIQAMHPSS---SRPDIYEIVALLHPR 775

RESULT 5
H70804
Hypochemical protein RV3494c - Mycobacterium tuberculosis (strain H37Rv)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C/Accession: H70804
R/Colo: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sultoni, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295981; PMID:9634230
A/Accession: H70804
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-564 <COL>
A/Cross-references: UNIPROT:O5533; GB:AL022022; GB:AL123456; NID:93261554; PDB:CA11773
A/Experimental source: strain H37Rv
C/Genetics:
A/Gene: RV3494c

Query Match 4.3%; Score 118; DB 2; Length 564;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 51; Conservative 18; Mismatches 51; Indels 80; Gaps 11;

QY 354 SLASVCDLF--TASNDPLMRFLYLDPRDNTVR--VQDTWKELYRK--HIQKESPK 408
D 343 SVRIPIIDMCKTAQNDP-----STVRGRANPCCOEPFGKAPVQLDRDR 389
QY 409 GRFWMLBSSHTHTPTFYNPLHPRPSSRLPQGITGSEYQRPPLPV 457
D 390 G-----YFVGTNTPRGPIPYGTEVTDGRNILPKNKP--YIRPGA-----DIDPGVPIV 438

QY 458 GDPISLIRPGGEMPSQ-----FPPLRPF----- 482
D 439 GPPPGQVAGFGAPBHDQACAPPPNDNGPPPTSMKPPGVPVPPVPAITPPPPP 498
QY 483 ----DPVGPLPGRPPIILPG 497
D 499 PEGTGPFGPAPGPQASG 518

RESULT 6
A41724
Limb deformity (ld) protein - chicken
C/Species: Gallus gallus (chicken)
C/Date: 04-Mar-1993 #sequence_revision 15-Aug-1997 #text_change 09-Jul-2004
C/Accession: S24286; S38780; A41724
R/Trump, A.; Blundell, P.A.; de la Pompa, J.L.; Zeller, R.
Genes Dev. 6, 14-28, 1992
A/Title: The chicken limb deformity gene encodes nuclear proteins expressed in specific
A/Reference number: A41724; MUID:92112031; PMID:1730407
A/Accession: S24286
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1213 <TRU>
A/Cross-references: UNIPROT:O05858; EMBL:X62681
A/Experimental source: embryo
R/Zeller, R.
submitted to the EMBL Data Library, August 1991
A/Reference number: S38780
A/Accession: S38780
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-885; A', 887-1213 <ZEL>
A/Cross-references: EMBL:X62681; NID:963567; PID:963568
C/Comment: Mutations in this gene affect morphogenesis of both limbs and kidneys.
C/Genetics:
A/Gene: ld
C/Keywords: nucleus

Query Match 4.3%; Score 117.5; DB 2; Length 1213;
Best Local Similarity 19.4%; Pred. No. 3.7;
Matches 105; Conservative 55; Mismatches 204; Indels 177; Gaps 19;

QY 57 TGDFTLASVGVSGDILCLTQDDIPRNPSTSDSHSLQNNQOPSLATSSN----- 111
D 297 TEDGTTTETIKPRENDLALKLRQPVKKSNTSGITTKKSSSEPRASFTLEQJSHLINT 356
QY 112 QTSMODEOPSPSPFOQAQSGVWNDMSLGPSQNFASIODNAHMAEGTFYSEPMLC 171
D 357 DVSKNDEFTQSGAGFGE-----TEDSDEGENVASGQ-----TEPLFP 395
QY 172 SESVSGQVPHSLFTLYQSDCSGDANDALIVLHL-----MESGYTPGTRA--KALSMPE 226
D 396 SEELKS-----SPASALDVKALFTRPKKETADPSELAIKRNENE 440
QY 227 KWLKSGVYKQYMHPLCEGSSATLTCVPL-----GNLIVNATLKNINIRSVKRLQL 279
D 441 KESLAVVERSKRKGDDPSDKSPDLSBEDDTPGLQVWPPPNRHS----- 491
QY 280 LPESFTCKKLGENVANIYKDLQKLSRLFKQOLVYVPLAFTROALNLPDVGVLVLEL 339
D 492 ----EYVGVGKYTEAEYQAAIHLKREHKE-----ITLKSQF 526
QY 340 KLIRFLDVRVSYSL-----SAVCDLFTASND-----PLLMRFL 376
D 527 ELRVHNGEVAVSTAQLEETIAHKNDLKNLRNREARDIGVSTEDDNLPTKYRVC 586
QY 377 LRDFDNTVRVQDTWKELYRKRIHQKESPKGRFWMLBSSHTHT----- 422
D 587 IQTDRETFIKSEENRANVKNQIVPK-----LNISSLTSHISITGCKNSYDVP 638
QY 423 -----PFYNPLHPRPSSRLPQGITGSEYQRPPLPVAGDPISSILP- 466
D 639 SESVUSCOPKQMLPSPPPPPPPPPPP-----PP-----PPPPPSDSLPGVLP 684


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QY 232 GYKLO--YMH-----PLCESSATLTCVPLGNLIVNATLKINNEISVKYKQLP 281
D 3519 GQQQQQVSLHTAGGGSHQGLSGSSSSSASV-----HLLAQPSVLGDPGNTQMLLGP 3575
QY 282 ESTICKEKLGENVANIKYKLOKLSRLFKDQVYPLLAFTROALNDPVFGVLLPLEKTL 341
D 3576 QQPMLEPRPMQNTGP-----QPPKPGPVL---QSGQGLP---GVGIMPTVQGL 3617
QY 342 RIRFLDVSATLSAVCRDPLFASNDPLMRFLYLRDRFRDNTVRQDIDMKELYKRI 401
D 3618 R---AQLQGVLAKNQQLRLSLPQQQQL-----QALLMQRL 3651
QY 402 QRKESPKGRFVMLP---SSTHTIPF-----YNP-----LHPRFPPS 436
D 3652 QQSCA-----VRQTPPYGEPGTQTSPLQGLLGCQPLGFPQGTGPLQELGAGPRFGP 3706
QY 437 SRL--PGIIGGEYDQRTLPYVG-----DPISLLPGPEPTPSQPPPLRPREDVGP 489
D 3707 PRLPAPGALS-----TGPVLGVPVHTPPSS--PQEPKPSQLPSSSQLPTEAQLP 3757
QY 490 GPNPILPGRGGNDPRFPFRPSRGRPTDGRLS 520
D 3758 PTHGTPKPGPGLTEPP--PGRVSPAAQLA 3786

RESULT 10
ALR protein - human
C/Species: Homo sapiens (man)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C/Accession: T03454
R/Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano,
Oncogene 15, 549-560, 1997
A/Title: Structure and expression pattern of human ALR, a novel gene with strong homolog
A/Reference number: Z14954; MUID:97388474; PMID:9247308
A/Accession: T03454
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-5262 <PRA>
A/Cross-references: UNIPROT:O14686; EMBL:AF010403; NID:92358284; PIDN:AAC51734.1; PID:92
C/Genetics:
A/Map position: 12
C/Superfamily: acute lymphoblastic leukemia protein, ALR type
C/Keywords: alternative splicing

```

Query Match 4.2%; Score 116; DB 2; Length 5262;

Best Local Similarity 20.0%; Pred. No. 41;

Matches 102; Conservative 64; Mismatches 181; Indels 164; Gaps 25;

QY 94 EHSLSLQNEPRLATSNQTSNQMDEQSDSFCQQAQS--GVNND-SYLGEPQNEALS 150

D 3661 QQQQLQQQQQQQQQLQQQQQQQQQQQQQQQQQQQQQLLQSGRTLLSPQQ----- 3714

QY 151 IODNAHMAEGTGFYPSHPM-----LCSESV----- 176

D 3715 -QQQQQVALBPM-PAKPLGHFSSPGALGPTLLTGKQNTVPANVSSEATEBSPTHQGG 3772

QY 177 ---GVPHSLFTLYQADCSANDALIVYIHLIMESGTPQ-GTEAKLSMPEKWKLS 231

D 3773 PLATGTPBEMATEPGEVKPSLSDSGLLVQ-----PQPPQPSLQQLQPPPLRP 3823

QY 232 GYVYLCQ--YMH-----PLCESSATLTCVPLGNLIVNATLKINNEISVKYKQLP 281

D 3824 GQQQQQVSLHTAGGGSHQGLSGSSSSSASV-----HLLAQPSVLGDPGNTQMLLGP 3880

QY 282 ESPTCKEKLGNVANIKYKLOKLSRLFKDQVYPLLAFTROALNDPVFGVLLPLEKTL 341

D 3881 QQPMLEPRPMQNTGP-----QPPKPGPVL---QSGQGLP---GVGIMPTVQGL 3922

QY 342 RIRFLDVSATLSAVCRDPLFASNDPLMRFLYLRDRFRDNTVRQDIDMKELYKRI 401

D 3923 R---AQLQGVLAKNQQLRLSLPQQQQL-----QALLMQRL 3956

```

QY 402 QRKESPKGRFVMLP---SSTHTIPF-----YNP-----LHPRFPPS 436
D 3957 QQSCA-----VRQTPPYGEPGTQTSPLQGLLGCQPLGFPQGTGPLQELGAGPRFGP 4011
QY 437 SRL--PGIIGGEYDQRTLPYVG-----DPISLLPGPEPTPSQPPPLRPREDVGP 489
D 4012 PRLPAPGALS-----TGPVLGVPVHTPPSS--PQEPKPSQLPSSSQLPTEAQLP 4062
QY 490 GPNPILPGRGGNDPRFPFRPSRGRPTDGRLS 520
D 4063 PTHGTPKPGPGLTEPP--PGRVSPAAQLA 4091

RESULT 11
hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: G66292
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Matzalli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A66141; MUID:21016719; PMID:11130712
A/Accession: G66292
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1006 <STO>
A/Cross-references: UNIPROT:Q9LMQ1; GB:AE005172; NID:9927662; PIDN:AA62153.1; GSPDB:GM
C/Genetics:
A/Map position: 1

```

Query Match 4.1%; Score 112; DB 2; Length 1006;

Best Local Similarity 32.7%; Pred. No. 7;

Matches 36; Conservative 6; Mismatches 48; Indels 20; Gaps 3;

QY 406 SPKGRFWMLPSSHTTTFYFNPPLHPRFPSSRLPGIIGGEYDQRTLPYVGPISLI 465

D 88 SPENPFLFPQ-----DRPPRPRPRPRPRP-----PLVPSBPPLH 128

QY 466 PGPETPSQFPPLRPDPVGPLPQPNPILPGRGPN-DRPFRPSRGRP 514

D 129 PRPSPCPPLMPSPPPLVSPPPPPPLVSPPPSPPPPPPPPPPPPPPPPPPPPPPP 178

RESULT 12

FB19 protein - human

C/Species: Homo sapiens (man)

C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C/Accession: J02021

R/Rotero, A.; Griffe, A.; Carella, M.; Rommens, J.M.; Valentino, M.A.; Roetto, A.; Zelante

Biochem. Biophys. Res. Commun. 250, 555-557, 1998

A/Title: Cloning of a new gene (FB19) within HLA class I region.

A/Reference number: J02021; MUID:99003493; PMID:9784381

A/Accession: J02021

A/Molecule type: mRNA

A/Residues: 1-940 <TOR>

A/Cross-references: UNIPROT:O00405; GB:Y13247; NID:92117158; PIDN:CAA73697.1; PID:9211715

C/Genetics:

A/Map position: 6p21.3

Query Match 4.0%; Score 111.5; DB 2; Length 940;

Best Local Similarity 36.8%; Pred. No. 6.9;

Matches 39; Conservative 6; Mismatches 40; Indels 21; Gaps 6;

QY 424 FYRPHLHPRPPSSRLPPGIIIGSEYDQRTLPYVGDPISSILPGRGETPSQFPRLPRFD 483
DB 643 FPPPGGGMPPGPHGG-PEGVPGRLLGPPPPRGDGFWD---GPGD-PMRGGMRG--- 694
QY 484 PVGFLPGFNPLPGRG-----PNDRFPPRSR-----GRPTDGR 518
DB 695 --GGGPGGPPHRRGGRGNGNPPPPPPPPFGAGCGSGGSGPPRGR 738

RESULT 13

T49187
hypothetical protein MAA21.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49187
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Nemes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, April 2000
A:Reference number: 225018
A:Accession: T49187
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1097 <R1E>
A:Cross-references: UNIPROT:Q9LY69; EMBL:AL163818; GSDB:GNC00061; ATSP:MAA21.90
A:Experimental source: cultivar Columbia; BAC clone MAA21
C:Genetics:
A:Gene: ATSP:MAA21.90
A:Map position: 3
A:introns: 106/2; 124/3; 165/3; 198/1; 210/2; 245/3; 265/1; 297/3; 337/3; 352/1; 394/1.

Query Match 4.0%; Score 111; DB 2; Length 1097;
Best Local Similarity 20.2%; Pred. No. 9.4;
Matches 111; Conservative 75; Mismatches 218; Indels 146; Gaps 26;
QY 37 TWG-----SSNRTFTLLNYKDLTDEETLASVGSDDLCLLLODD-IPAPN 86
DB 435 TWGLKIMFEEBEGSRKTLISHLGFTLPVAKQAVG---LSDDLNGIHLDTADALD 491
QY 87 IPSSTDESHSLQNNQ-----PSLANSSNOTSNODEPSPD--SFOGQAAGGWNDD 138
DB 492 LDDNENEAAMFMDNGEFPNNFPAPKPTPVSTAKDMPSTDTFSTGEETQEMOEEREE 551
QY 139 MLGP-----SCNFEASIDON--AHMAGTGFYPS--EPMLCSES 174
DB 552 SSDVFNDAIQRALIVGDYKAVDQCITANKADALVIAHG-CTALMBESTREKYLKTS 610
QY 175 -----VEGVPHSLFTLYOSADCSANDALIYVLIHLMDESGYIPQGTAKALSMPEKV 228
DB 611 APYKVVSAVAVNNDLRSLIYRSHKFWKMTLLALC-----TPAQGEQW 653
QY 229 KLSGVYKIQYHNPICGSSATLTCPVPGN-LIIVNATLKINNEIRSYKRLQLLPESTICK 287
DB 654 T-----TLCDALASKL--MAAGNTLAAVLICYICAGVDRIVE---TWSRSLAN 696
QY 288 EKLGENVANIYKDLQKSLRFKDLVYPLA---FTROALNLPDVGVLVLP---LELK 340
DB 697 ERDRSVAHELLQDLMEXK-----LVIALATGNKKFASIOKLPESVAHELLAAGULLTTA 750
QY 341 LRIIRLLD-----VNSVLSLAVCRDLPLFAS-----NDPLMRFLYLR 378
DB 751 MKYKVLVDSGSLSPELSLIRDRISLSAEPETNTTASONTQPOSTMPYNOGPTQAQPVNLA 810
QY 379 DFRONTYVADDTWKELEYRKSHIORKESPKGRFVYLLPSTHTIP---FPPNPLHPRFP 425
DB 811 NPYNOVQOQPTDSYVQVSH-----PPMOQPTMPPHQAQPARQDSFTFPAFT-SNAOP 864
QY 436 SSR-----LPPGIIGGEYDQRTLPYVGDPISSILPGRGETPSQFPRLPRDPVGPL- 488
DB 865 SMRTTFVYSTPALAKNADYQOQPTMS-----SHSFTGSPNNNAVPPVPGGYAFSGPSQ 918
QY 489 --GPNPLP 496
DB 919 LGQYFNPGRP 928

RESULT 14

S57447
HPRRII-7 protein - human
N:Alternate names: HPRRII-4 protein
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C:Accession: S57447; S57489
R:Pleischauer, K.L.
submitted to the EMBL Data Library, June 1992
A:Reference number: S57447
A:Accession: S57447
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-551 <FLB>
A:Cross-references: UNIPROT:Q16630; EMBL:X67336; NID:g871300; PIDN:CAA47752.1; PID:g87130
A:Accession: S57489
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-551 <FL2>
A:Cross-references: EMBL:X67337; NID:g871298; PIDN:CAA47752.1; PID:g871299
C:Genetics:
A:introns: 231/3
A:Superfamily: ribonucleoprotein repeat homology
F:82-151/Domain: ribonucleoprotein repeat homology <RNM4>

Query Match 4.0%; Score 110.5; DB 2; Length 551;
Best Local Similarity 31.1%; Pred. No. 3.7;
Matches 41; Conservative 9; Mismatches 39; Indels 43; Gaps 8;
QY 408 KGRFVMLPSSGTHITPPYPNPL---HPRPPSSRLPPGIIIGSEYDQRTLPYVGDPISS 463
DB 204 RGRFPQAVPQGGDR-----PPGAPGCGPPPPPAQGTTP-----RPPGPPGPPPP 250
QY 464 LIPGPGET---PSCGPPPLR-----PRFDVGPL-PGPNPLPGRGQPN 502
DB 251 GPPPPGQVLPPPLAPPPKGRDRPPPPVLPFGQPPGCP---PLGFLPQPPPPPVGYGPP 307
QY 503 DRFPFRPSGRP 514
DB 308 G--PPPPQGGPP 317

RESULT 15

A54964
spliceosome-associated protein SAP-49 - human
C:Species: Homo sapiens (man)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: A54964
R:Champion-Arnard, P.; Reed, R.
Genes Dev. 8; 1974-1983, 1994
A:Title: The prespliceosome components SAP 49 and SAP 145 interact in a complex implicat
A:Reference number: A54964; MUID:95047348; PMID:7958871
A:Accession: A54964
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-424 <CHA>
A:Cross-references: UNIPROT:Q15427; GB:U35013; NID:g556216; PIDN:AAA60300.1; PID:g556217
C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein
F:14-61/Domain: ribonucleoprotein repeat homology <RNM4>
F:101-169/Domain: ribonucleoprotein repeat homology <RNM2>

Query Match 4.0%; Score 110; DB 2; Length 424;
Best Local Similarity 32.0%; Pred. No. 2.8;
Matches 39; Conservative 9; Mismatches 32; Indels 42; Gaps 9;
QY 430 HPRPPSSRLP-PGI-----IG-----GEYDQRTLPYVGDPISSILPGRG 469
DB 292 HPRPPGGMPPRPGSQQLAHNGPHGIGHAGPPGSGCGPPPPRPPG-----MPHFG 345
QY 470 HPRPPPLPRPF-PPV---GFLP-----GPNPLPGRG---GPNDRFPFRPSRG-----R 513

Db	346	PPNMGMPRRGPPGSEVNGHFGZMPPHQMGPPPLMPPHGTYTGP	PPPPYIGYQRGPLPPR	405
QY	514	PT	515	
Db	406	PT	407	

Search completed: November 16, 2004, 07:21:58
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 06:56:04 ; Search time 202 Seconds

(Without alignments)
1486.859 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 2754
Sequence: 1 MRLRVRLKRTWPLEVPETE.....DRFPFRSGRPTDGLSLFM 522

Scoring table: BIOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2748	99.8	522	1 FBX7_HUMAN	Q9Y311 homo sapien
2	2748	99.8	522	2 CAG30377	Cag30377 homo sapi
3	1977.5	71.8	523	2 Q8K0A5	Q8K0A5 mus musculu
4	1295	47.0	361	2 Q6Y0L7	Q6Y0L7 gallus gall
5	1295	47.0	361	2 AAP83452	AAP83452 gallus ga
6	1125	40.8	478	2 Q6DE59	Q6DE59 xenopus lae
7	240.5	8.7	475	2 Q9ZUB8	Q9ZUB8 arabidopsis
8	205	7.4	776	2 Q8GZU6	Q8GZU6 oryza sativ
9	187.5	6.8	350	2 Q9ZUB9	Q9ZUB9 arabidopsis
10	147	5.3	270	1 PSF1_DROME	Q9V633 drosophila
11	145.5	5.3	434	2 Q9Y593	Q9Y593 homo sapien
12	145.5	5.3	447	2 Q9NT57	Q9NT57 homo sapien
13	144	5.2	403	2 Q6PKH7	Q6PKH7 homo sapien
14	144	5.2	403	2 AAH00650	Aah00650 homo sapi
15	144	5.2	447	1 FBX9_HUMAN	Q9UK37 homo sapien
16	138.5	5.0	386	2 Q7Z1T2	Q7Z1T2 brachydanio
17	135	4.9	436	2 Q8VDV6	Q8VDV6 mus musculu
18	135	4.9	436	2 Q8BK06	Q8BK06 mus musculu
19	134.5	4.9	1183	2 Q7TSH6	Q7TSH6 mus musculu
20	134.5	4.9	1209	2 Q6PFR0	Q6PFR0 mus musculu
21	134.5	4.9	1209	2 AAH57592	Aah57592 mus muscu
22	134	4.9	3148	2 Q8H608	Q8H608 poncirus tr
23	129	4.7	745	2 Q6Z125	Q6Z125 oryza sativ
24	128.5	4.7	850	2 BAD03549	Bad03549 oryza sat
25	128.5	4.6	431	2 O17055	O17055 caenorabadi
26	126.5	4.6	355	2 Q7SY92	Q7SY92 xenopus lae
27	126	4.5	271	1 PSF1_HUMAN	Q96955 homo sapien
28	123	4.5	271	1 PSF1_HUMAN	Q92510 homo sapien
29	123	4.5	936	2 Q8QR77	Q8QR77 chimpanzee
30	122	4.4	936	2 Q6MB50	Q6MB50 parachlamyd
31	122	4.4	953	2 CAF24199	Caif24199 parachlam

Result	Score	Query Match	Length	ID	Description
32	120.5	4.4	888	2 Q6P9Q5	Q6P9Q5 mus musculu
33	120.5	4.4	888	2 AAH60652	Aah60652 mus muscu
34	120.5	4.4	911	2 Q8CIE2	Q8CIE2 mus musculu
35	120.5	4.4	925	2 Q8NFE4	Q8NFE4 homo sapien
36	120	4.4	271	2 Q8BHL8	Q8BHL8 m mus muscu
37	120	4.4	684	1 CDC4_CANAL	P53699 candida alb
38	120	4.4	1255	2 Q9R2J6	Q9R2J6 plasmid col
39	119	4.3	271	2 Q8C0G9	Q8C0G9 mus musculu
40	119	4.3	287	2 Q95UG5	Q95UG5 babesia bov
41	119	4.3	844	2 Q9R2J5	Q9R2J5 plasmid col
42	118	4.3	442	2 Q9VG61	Q9VG61 drosophila
43	118	4.3	564	2 Q53539	Q53539 mycobacteri
44	118	4.3	564	2 Q7WMD7	Q7WMD7 mycobacteri
45	117.5	4.3	503	1 WARP_HUMAN	Q43516 homo sapien

ALIGNMENTS

Result	Score	Query Match	Length	ID	Description
1	2748	99.8	522	1 FBX7_HUMAN	Q9Y311 homo sapien
2	2748	99.8	522	2 CAG30377	Cag30377 homo sapi
3	1977.5	71.8	523	2 Q8K0A5	Q8K0A5 mus musculu
4	1295	47.0	361	2 Q6Y0L7	Q6Y0L7 gallus gall
5	1295	47.0	361	2 AAP83452	AAP83452 gallus ga
6	1125	40.8	478	2 Q6DE59	Q6DE59 xenopus lae
7	240.5	8.7	475	2 Q9ZUB8	Q9ZUB8 arabidopsis
8	205	7.4	776	2 Q8GZU6	Q8GZU6 oryza sativ
9	187.5	6.8	350	2 Q9ZUB9	Q9ZUB9 arabidopsis
10	147	5.3	270	1 PSF1_DROME	Q9V633 drosophila
11	145.5	5.3	434	2 Q9Y593	Q9Y593 homo sapien
12	145.5	5.3	447	2 Q9NT57	Q9NT57 homo sapien
13	144	5.2	403	2 Q6PKH7	Q6PKH7 homo sapien
14	144	5.2	403	2 AAH00650	Aah00650 homo sapi
15	144	5.2	447	1 FBX9_HUMAN	Q9UK37 homo sapien
16	138.5	5.0	386	2 Q7Z1T2	Q7Z1T2 brachydanio
17	135	4.9	436	2 Q8VDV6	Q8VDV6 mus musculu
18	135	4.9	436	2 Q8BK06	Q8BK06 mus musculu
19	134.5	4.9	1183	2 Q7TSH6	Q7TSH6 mus musculu
20	134.5	4.9	1209	2 Q6PFR0	Q6PFR0 mus musculu
21	134.5	4.9	1209	2 AAH57592	Aah57592 mus muscu
22	134	4.9	3148	2 Q8H608	Q8H608 poncirus tr
23	129	4.7	745	2 Q6Z125	Q6Z125 oryza sativ
24	128.5	4.7	850	2 BAD03549	Bad03549 oryza sat
25	128.5	4.6	431	2 O17055	O17055 caenorabadi
26	126.5	4.6	355	2 Q7SY92	Q7SY92 xenopus lae
27	126	4.5	271	1 PSF1_HUMAN	Q96955 homo sapien
28	123	4.5	271	1 PSF1_HUMAN	Q92510 homo sapien
29	123	4.5	936	2 Q8QR77	Q8QR77 chimpanzee
30	122	4.4	936	2 Q6MB50	Q6MB50 parachlamyd
31	122	4.4	953	2 CAF24199	Caif24199 parachlam

RA Roe B.A., Chen F., Chu L., Gibbtree U., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Lob P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren C., Shaul S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhao M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozerky P., Rohlfing T.,
RA Schaefer P., Walker C., Mansley A., Wohlmann P., Papin K., Nelson J.,
RA Korfi I., Bedell U.A., Hillier L.M., Marais E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurashiki H., Salta S.,
RA Budarf M.L., McEwen D.H.E., Johnson A., Wong A.C.C., Morrow B.B.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dunancki D.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenleitch A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
RN
RP
RP
RC TISSUE=Pancreas;
RX MEDLINE=23386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Butlow K.H., Schneider C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heselt F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshitsuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abrahamson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunnatrine P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Polity S.W.,
RA Villalón D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalski U., Smallus D.E.,
RA Schnerch A., Schain J.E., Jones S.J.W., Marra W.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -I- FUNCTION: Probably recognizes their ubiquitination and degradation
CC proteins and promotes their ubiquitination and degradation.
CC -I- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
CC (by similarity).
CC -I- SIMILARITY: Contains 1 F-box domain.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC
DR EMBL; AF129537; AAF04471.1; -
DR EMBL; AF233225; AAF67155.1; -
DR EMBL; AL050253; CAB43356.1; -
DR EMBL; Z71183; CAB63143.1; -
DR EMBL; BC008361; AAH08361.1; -
DR Genew; HGNC:13586; FBXO7.
DR MTM; 605648; -
DR GO; GO:0000151; C:ubiquitin ligase complex; TAS
DR GO; GO:0004844; F:ubiquitin-protein ligase activity; TAS.
DR GO; GO:0005611; P:ubiquitin-dependent protein catabolism; TAS.
DR InterPro; IPRO01810; F-box.
DR InterPro; IPRO08945; Skp1_Skp2.
DR Pfam; PF00646; F-box_1.
DR PROSITE; PSS0181; FBXX_1.
KW ubl conjugation pathway.
FT DOMAIN 329 375 F-box.

Accession	Species	Length	Score	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414	DB 415	DB 416	DB 417
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SQ SEQUENCE 522 AA; 58502 MW; CAESE70A0747287A CRC64;
 Query Match 99.8%; Score 2748; DB 2; Length 522;
 Best Local Similarity 99.8%; Pred. No. 2e-175;
 Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLVRLIKRTWPLEVEPTETPTLGHLSHRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60
 DB 1 MRLVRLIKRTWPLEVEPTETPTLGHLSHRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60
 QY 61 ETLASGYVSGDLICLILQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNQTSMDQEP 120
 DB 61 ETLASGYVSGDLICLILQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNQTSMDQEP 120
 QY 121 SDSFGQAAGSGVWVNDSDMLGPSQNFESAESIQDNAHMAEGTGFPSEPMCSSEVSGQVP 180
 DB 121 SDSFGQAAGSGVWVNDSDMLGPSQNFESAESIQDNAHMAEGTGFPSEPMCSSEVSGQVP 180
 QY 181 HSLFTLYQSADCSANDALIVLHLMLESGYIPQGTBAVALSMPEKMKLSGVYKLYQYH 240
 DB 181 HSLFTLYQSADCSANDALIVLHLMLESGYIPQGTBAVALSMPEKMKLSGVYKLYQYH 240
 QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVYKRLQLLPESPICKKLGENVANITYD 300
 DB 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVYKRLQLLPESPICKKLGENVANITYD 300
 QY 301 LQKLSRLFKQQLVYPLIAFTROALNPDVFGVLVPLLELKLRIFRLLDVRSVLSAVCR 360
 DB 301 LQKLSRLFKQQLVYPLIAFTROALNPDVFGVLVPLLELKLRIFRLLDVRSVLSAVCR 360
 QY 361 DLFTASNDPLMLRLVYDRDNTVRVQDDMKELVYKRIQKESKGFVWLLSSSTH 420
 DB 361 DLFTASNDPLMLRLVYDRDNTVRVQDDMKELVYKRIQKESKGFVWLLSSSTH 420
 QY 421 TIFPYPNLHPRPSPSSRLPGIIGGEYDQRPPLPYVGDPISSILPGSGETPSQFPPLRP 480
 DB 421 TIFPYPNLHPRPSPSSRLPGIIGGEYDQRPPLPYVGDPISSILPGSGETPSQFPPLRP 480
 QY 481 RPDVPVGLPGPNPILPGRGPNDRFPFRPSRGRPTDGRLSFW 522
 DB 481 RPDVPVGLPGPNPILPGRGPNDRFPFRPSRGRPTDGRLSFW 522

RESULT 3
 OQK0A5 PRELIMINARY; PRT; 523 AA.
 AC OQK0A5;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE F-box only protein 7.
 GN Name=F-box; 7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RX MEDLINE=2388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marziani K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein J., Uehli T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mollati S.J.,
 RA Bosak S.A., Morley P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maita M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RA Strausberg R.,
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC032153; AAH32153.1; -
 DR MGI; MGI:1917004; Fbox07.
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 DR PROSITE; PS50181; FBOX; 1.
 SQ SEQUENCE 523 AA; 57634 MW; ABFD250070C1FEB5 CRC64;
 Query Match 71.8%; Score 1977.5; DB 2; Length 523;
 Best Local Similarity 72.5%; Pred. No. 7e-124;
 Matches 380; Conservative 56; Mismatches 85; Indels 3; Gaps 3;

QY 1 MRLVRLIKRTWPLEVEPTETPTLGHLSHRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60
 DB 1 MRLVRLIKRTWPLEVEPTETPTLGHLSHRLSLCTWGYSSNTRFTITLNNKALITGDE 60
 QY 61 ETLASGYVSGDLICLILQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNQTSMDQEP 120
 DB 61 ETLASGYVSGDLICLILQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNQTSMDQEP 120
 QY 121 SDSFGQAAGSGVWVNDSDMLGPSQNFESAESIQDNAHMAEGTGFPSEPMCSSEVSGQVP 180
 DB 121 SDSFGQAAGSGVWVNDSDMLGPSQNFESAESIQDNAHMAEGTGFPSEPMCSSEVSGQVP 180
 QY 181 HSLFTLYQSADCSANDALIVLHLMLESGYIPQGTBAVALSMPEKMKLSGVYKLYQYH 240
 DB 181 HSLFTLYQSADCSANDALIVLHLMLESGYIPQGTBAVALSMPEKMKLSGVYKLYQYH 240
 QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVYKRLQLLPESPICKKLGENVANITYK 299
 DB 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVYKRLQLLPESPICKKLGENVANITYK 299
 QY 300 DLQKLSRLFKQQLVYPLIAFTROALNPDVFGVLVPLLELKLRIFRLLDVRSVLSAVC 359
 DB 300 DLQKLSRLFKQQLVYPLIAFTROALNPDVFGVLVPLLELKLRIFRLLDVRSVLSAVC 360
 QY 360 RDLFTASNDPLMLRLVYDRDNTVRVQDDMKELVYKRIQKESKGFVWLLPESST 419
 DB 361 HDLFTASNDPLMLRLVYDRDNTVRVQDDMKELVYKRIQKESKGFVWLLPESST 419
 QY 420 HTIFPYPNLHPRPSPSSRLPGIIGGEYDQRPPLPYVGDPISSILPGSGETPSQFPPLRP 478
 DB 420 HTIFPYPNLHPRPSPSSRLPGIIGGEYDQRPPLPYVGDPISSILPGSGETPSQFPPLRP 479
 QY 479 RPRPVPVGLPGPNPILPGRGPNDRFPFRPSRGRPTDGRLSFW 522
 DB 480 RPRPVPVGLPGPNPILPGRGPNDRFPFRPSRGRPTDGRLSFW 523

RESULT 4
 OQ6Y0L7 PRELIMINARY; PRT; 361 AA.
 AC OQ6Y0L7;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE F-box only protein 7 (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;

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RN [1]
RP SEQUENCE FROM N.A.
RA Bhadra M.G., Kim H.
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY194289; AAP83452.1; JOINED.
DR EMBL; AY194288; AAP83452.1;
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PSS0181; FBOX; 1.
FT NON_TER
SQ SEQUENCE 361 AA; 40110 MW; 51C54C0292833884 CRC64;

Query Match 47.0%; Score 1295; DB 2; Length 361;
Best Local Similarity 65.6%; Pred. No. 1,9e-78;
Matches 246; Conservative 47; Mismatches 62; Indels 20; Gaps 4;

QY 153 DNAAHAGCTGFPSEPMKCSSEVGVPHSLEITLYGSAACSDANDALIVLHILMLESGY 212
DB 2 EDVDLEGTGSPSEPMKCSSEADGELPHSLEVLITSAECTSATDALIVLHILMETGY 61
QY 213 IPQGTAKALSMPEKMKLGVYKLYVHPVLCGSSATLTCVPLGNLIVNATLKINNEIR 272
DB 62 VPQGTAKAYSMPEKMKNGVYKLYTHPLCEBSSAGLTCVPLGDLVAIVATLKINREIK 121
QY 273 SVKRLQLLPESFICKKELGENVANIYKDLQKLSLFFDQVYPLATRQALNLPDYFGL 332
DB 122 GVKRIQLLPASFVFCQE-PEKAVAGYKDLQKLSLFFDQVYSLAARQALNLPDYFGL 180
QY 333 VVLPELKLRIPLLDVRSVLSISAVCRDLFTASNDPLMRFLYLRFDRNTAVQDTPW 392
DB 181 VVLPELKLRIPLLDVRSVLSISAVCRDLFTASNDPLMRFLYLRFDRNTAVQDTPW 227
QY 393 KELYRKRIHQKESPKGRFVMLPSSTHTIPFYNPPLHPFPSPSRUP-----PGLTIGE 447
DB 228 SELYKKLQKKKEALRWKH-MFLPPTPIPIPHFNPPSPFPNPPSPNIPYPMWIGE 286
QY 448 YDQRTPLPYVDPISSLLPGSGETPSPQPPPLRPPFDVGPPLPGNPPLIPGRGNDPFP 507
DB 287 YGERPTLLYIGDPIINSLLPGGEAPGQPPPRPHDPGLSGANPPLPGAGSDPFP 346
QY 508 RPSRGRPTDGRLSFM 522
DB 347 RPSRGRPTDVRRAFI 361

RESULT 5
AAP83452 PRELIMINARY; PRT; 361 AA.
AC AAP83452;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE F-box only protein 7 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN NCBI_TaxID=9031;
RP SEQUENCE FROM N.A.
RA Bhadra M.G., Kim H.
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY194288; AAP83452.1; JOINED.
DR EMBL; AY194289; AAP83452.1;
FT NON_TER
SQ SEQUENCE 361 AA; 40110 MW; 51C54C0292833884 CRC64;

Query Match 47.0%; Score 1295; DB 2; Length 361;
Best Local Similarity 65.6%; Pred. No. 1,9e-78;
Matches 246; Conservative 47; Mismatches 62; Indels 20; Gaps 4;

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QY 153 DNAAHAGCTGFPSEPMKCSSEVGVPHSLEITLYGSAACSDANDALIVLHILMLESGY 212
DB 2 EDVDLEGTGSPSEPMKCSSEADGELPHSLEVLITSAECTSATDALIVLHILMETGY 61
QY 213 IPQGTAKALSMPEKMKLGVYKLYVHPVLCGSSATLTCVPLGNLIVNATLKINNEIR 272
DB 62 VPQGTAKAYSMPEKMKNGVYKLYTHPLCEBSSAGLTCVPLGDLVAIVATLKINREIK 121
QY 273 SVKRLQLLPESFICKKELGENVANIYKDLQKLSLFFDQVYPLATRQALNLPDYFGL 332
DB 122 GVKRIQLLPASFVFCQE-PEKAVAGYKDLQKLSLFFDQVYSLAARQALNLPDYFGL 180
QY 333 VVLPELKLRIPLLDVRSVLSISAVCRDLFTASNDPLMRFLYLRFDRNTAVQDTPW 392
DB 181 VVLPELKLRIPLLDVRSVLSISAVCRDLFTASNDPLMRFLYLRFDRNTAVQDTPW 227
QY 393 KELYRKRIHQKESPKGRFVMLPSSTHTIPFYNPPLHPFPSPSRUP-----PGLTIGE 447
DB 228 SELYKKLQKKKEALRWKH-MFLPPTPIPIPHFNPPSPFPNPPSPNIPYPMWIGE 286
QY 448 YDQRTPLPYVDPISSLLPGSGETPSPQPPPLRPPFDVGPPLPGNPPLIPGRGNDPFP 507
DB 287 YGERPTLLYIGDPIINSLLPGGEAPGQPPPRPHDPGLSGANPPLPGAGSDPFP 346
QY 508 RPSRGRPTDGRLSFM 522
DB 347 RPSRGRPTDVRRAFI 361

RESULT 6
Q6D59 PRELIMINARY; PRT; 478 AA.
AC Q6D59;
DT 01-OCT-2004 (TREMBlrel. 28, Created)
DT 01-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
RN NCBI_TaxID=8355;
RP SEQUENCE FROM N.A.
RA MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richards P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative."
RL Dev. Dyn. 225:384-391 (2002).

RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RC PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffler C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strauberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RM EMBL: BC077283; AAF77283.1;
 KW Hypothetical protein.
 SQ SEQUENCE 478 AA; 53251 MW; 8C12F01332C1873F CRC64;
 Query Match 40.8%; Score 1125; DB 2; Length 478;
 Best Local Similarity 47.5%; Pred. No. 6.5e-67;
 Matches 251; Conservative 74; Mismatches 147; Indels 56; Gaps 14;
 QY 1 MLRLVRLKRTWPLEVEPTETPTLGHLSHLRLSLCTWGSNTPTITLNYKDTGDE 60
 DB 1 MKLRVRKQTSRLLEAEQPTLGLDRSKLSVTLPSLGSATHTFTITNGDALTEQ 60
 QY 61 ETIASYGVIGDILICLILQD--DIPAPNIPSTPSEHSJONNEOPSATSSNQTSMODE 118
 DB 61 TTLESATIIISGDLIVLLPPSPQAPAPBERD-PRCPLEDPQP-----CSTANK 111
 QY 119 QPSDSFGQAAGQGVWMDSNLGPSONFEASIQDNAMAEGTGFYPS-EPMLCSSEVQ 177
 DB 112 RP---KGHADNKG-----GAMPQAEASPSLIDVAM-EGQLSGPAWEVMLCSBAVDG 159
 QY 178 QVPHSLLETLVQASDCSANDALITLILMLSEGYIQGTAEALSMPEKMSGYKQ 237
 DB 160 KIPHSLEVLVQLTASCSASDAFIVLHLMLEGTGLKGETALCPWRMRSGAYRLH 219
 QY 238 YMHPLCEGSSATLTCVPLGNLIVNATLKTINNEIRSYKRLQLPESFICEKLGENVANI 297
 DB 220 YTHPLCAEVSATLVCPLMGKLVIIATMTKINSEKSKYKQLLTINYSISPEPDNNVASG 279
 QY 298 YKDLQKSLFKQOLVPLAFTFOALNPDVGLVTLPELKLRIPLRIDVASVLSGA 357
 DB 280 YKDLQKSLGQKQVAPPLAAAGVNLDPVGLVTLPELKLRIPLRIDVLSLNTLSA 339
 QY 358 VCRDLFTASNDPLIMRELTYLRFEDNTVRVQDTMKELYKRIORKESEPKGSFV---ML 414
 DB 340 TCKELADLTDPSLMRFLCIRDFNSLPRLGTDWKLKYEKKQKMD-RNFVVRQEL 397
 QY 415 LPSTATITPIYPNPLHPRPSSSLPPGIIGGEYDQRPILPYGDPISLIPGGETPQ 474
 DB 398 PPRNAHYPIYPN-VFP---PDINYPGIIIGGDYDQRPPIV-----NPTH 440
 QY 475 FPLPRPFDVGLPGNPILPGCGNDRFPFRPSGRPTDGLSPM 522
 DB 441 LNP-----FKVTLPPSENDPSIPGSSG-----LRPSRGRLDIRRGFI 478
 RESULT 7
 Q9ZUB8 PRELIMINARY; PRT; 475 AA.
 AC Q9ZUB8;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE F508_33 protein (A1923780/F508_31).
 GN Name=F508_33;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC [1]
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vysotskaya V.S., Schwartz J.R., Yu G., Toriumi M., Liu S., Lenz C.,
 RA Li J., Kremenkova I., Luros J., Altafi H., Gonzalez A., Araujo R.,
 RA Buehler E., Com L., Conway A.B., Dunn P., Hansen N., Hultzer L.,
 RA Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W.,
 RA Ecker J.R., Federspiel N.A., Theologis A.;

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Theologis;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Barth J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
 RA Hsuan Y.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.X., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Shinzaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.,
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC005990; AAC98033.1;
 DR EMBL: AY045291; AAK83633.1;
 DR EMBL: AY145929; AAN31083.1;
 DR PIR: A86372; A86372.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR002052; N6_Mtase.
 DR InterPro: IPR008945; Skp1_Skp2.
 DR Pfam: PF00646; F-box; 1.
 DR SMART: SM00256; FBOX; 1.
 DR PROSITE: PS00181; FBOX; 1.
 DR PROSITE: PS00092; N6_Mtase; UNKNOWN 1.
 SQ SEQUENCE 475 AA; 52947 MW; D068CF15448FC3 CRC64;
 Query Match 8.7%; Score 240.5; DB 2; Length 475;
 Best Local Similarity 24.5%; Pred. No. 9.5e-06;
 Matches 116; Conservative 89; Mismatches 177; Indels 91; Gaps 20;
 QY 1 MLRLVRLKRTWPLEVEPTETPTLGHLSHLRLSLCTWGSNTPTITLNYKDTG 58
 DB 3 LRLRHETRETLKELADAD-TLHDLRRINPTV-----PSSVHLSLRKBLITPS 53
 QY 59 DEETLASGVIGDILICLILQDDIPAPNIPSTPSEHSJONNEOPSATSSNQTSMODE 118
 DB 54 PEDTLRSGLISGDLIYSLR-----AGESNMKLSDBSTVASQSSSNQTSVAD- 102
 QY 119 QPSDSFGQAAGQGVWMDSNLGPSONFEASIQDNAMAE--TGFPSPM----- 169
 DB 103 --SIGF-----AEVDVPPQAKSNP-----TSVE-----PEGDLSGMGPPEVDEQLM 147
 QY 170 --LCESEVGOVPHSLT--LYQADGSDANDALIVLHLMBSGYT--DQTE----- 218
 DB 148 ELAAGSRLESEFPFLKNILKEKSDTSELT-TTALSVHAWMLSGFVLNHNKSDKFNFS 206
 QY 219 AKALSPKRWKLSGVYKQVNHPLCEGSSATLTCVPLGNLIVNATL-----KINNE-- 271
 DB 207 KELTVSIRITLPELIKQNTNTI---ESVVKQNLPPVVVVGVIGSSGRVHANNLDK 263
 QY 272 -RSVRLQLPESFICEKLGENVANIYKDLQKSLFKQOLVPLAFTFOALNPDV 330
 DB 264 RRFVVIDLVMDTSTSD--EGSSIRYEVFMFRWYKDLVLPILIGICDXAGLEBP 320
 QY 331 GLVPLPLKLRIFPLDVRSVLSISANCRLDPLFASNDPLMRPLYLRFDFDNTVRV--Q 388
 DB 321 CLMRPLPLKRLIELLGVASIGNACVCTMRVYASNDLMKQCLAEVNNPVVTEAGD 380
 QY 389 DTDWK-----ELVYKRRIORKESEPKGRFVMLPPSTHTIIP 424

Db 381 SVNKKARFATFWKOLAAASDFWRQNLGRNISTSGIRFFRPIIGDPF 433

RESULT 8

Q8GZV6 PRELIMINARY; PRT; 776 AA.

AC Q8GZV6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein O1017C11.10.
GN Name=O1017C11.10;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriales; Oryzaeae; Oryza.
NCBI_TaxID=39947;

RP SEQUENCE FROM N.A.
RA Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
RA Collura K.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC135157; AAC00689.1; -

DR Gramene; Q8GZV6; -
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001092; HLH_Basic.
DR InterPro; IPR002029; Pept_S8_S53.
DR InterPro; IPR008945; Skp1_Skp2.
DR InterPro; IPR00626; Ubiquitin.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00213; UBO; 1.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
DR PROSITE; PS50053; UBQUITIN_2; 1.
DR Hypothetical protein.
KM SEQUENCE 776 AA; 83902 MW; F05B3429D2B924BD CRC64;

Query Match 7.4%; Score 205; DB 2; Length 776;
Best Local Similarity 22.0%; Pred. No. 4,5e-05;
Matches 115; Conservative 90; Mismatches 197; Indels 120; Gaps 25;

QY 1 MRLRLRLK-----TWLEPEREPTLGHRLSLRLSLCTGSGSNTFFITLN 51
Db 1 MRLRLRLK-----TWLEPEREPTLGHRLSLRLSLCTGSGSNTFFITLN 58
QY 52 YKDP-LTGD-EETLASYGIVSGDILCLIDDPAPNIPSTDESHSLQNN--EQPSL 106
Db 52 YKDP-LTGD-EETLASYGIVSGDILCLIDDPAPNIPSTDESHSLQNN--EQPSL 106
QY 59 RSEHLLTDPKATILPALGLASGDLLYFTL-SPLSPSPFPQOPQAPLPENPDPVPSI 117
Db 59 RSEHLLTDPKATILPALGLASGDLLYFTL-SPLSPSPFPQOPQAPLPENPDPVPSI 117
QY 107 ATSSNQTSMDQPSDPSFOGAASG---VWNDSTMIGSQNFSEASIDNMAAGTG 162
Db 107 ATSSNQTSMDQPSDPSFOGAASG---VWNDSTMIGSQNFSEASIDNMAAGTG 162
QY 118 AGAAPRTKSPVESGSSSMPQALCTNPGIPVASDPHHPP-----DYVMAAFA 166
Db 118 AGAAPRTKSPVESGSSSMPQALCTNPGIPVASDPHHPP-----DYVMAAFA 166
QY 163 FYPSPMLCSBVEGQVPHSLLELYQSAD-----CSDANDALIVLHLMLESGYIPQTE 218
Db 163 FYPSPMLCSBVEGQVPHSLLELYQSAD-----CSDANDALIVLHLMLESGYIPQTE 218
QY 167 VIKSR-----SLVVDGTREKEMEN--GADGTVC-----RLVVAHMAIDAGLIVANPV 216
Db 167 VIKSR-----SLVVDGTREKEMEN--GADGTVC-----RLVVAHMAIDAGLIVANPV 216
QY 219 AKALSMPEKMKLSGVY---KLQYMP-----LCEGSSATLTCPVLGNLIVNATLKI 267
Db 219 AKALSMPEKMKLSGVY---KLQYMP-----LCEGSSATLTCPVLGNLIVNATLKI 267
QY 217 GSCGLPQNM-ASGSEFVPMKYTLPELVEALPVVEGMAVAVLVSLNGNPMAYG--HV 273
Db 217 GSCGLPQNM-ASGSEFVPMKYTLPELVEALPVVEGMAVAVLVSLNGNPMAYG--HV 273
QY 268 NNEIISVRL-----QLPESFICKKUGENVANIYKDLQSLSPFQDLVYPLLATRQ 322
Db 268 NNEIISVRL-----QLPESFICKKUGENVANIYKDLQSLSPFQDLVYPLLATRQ 322
QY 274 PGATSGVRLCLDELAPLPLVDSDEVSTABE--REIHELMKVLKDEMCLPLMISLCQ 330
Db 274 PGATSGVRLCLDELAPLPLVDSDEVSTABE--REIHELMKVLKDEMCLPLMISLCQ 330
QY 323 ALNLPDVGIVLPLELKLRIPLRLDVASVLSLAVCRDLFTASNDPLMFLYLIRFRD 382
Db 323 ALNLPDVGIVLPLELKLRIPLRLDVASVLSLAVCRDLFTASNDPLMFLYLIRFRD 382
QY 331 LNNLSLPCIMALPDVAVAKVLEFVPGVDLARVQCTCKELRLADNLVAKKCEMEF-- 386
Db 331 LNNLSLPCIMALPDVAVAKVLEFVPGVDLARVQCTCKELRLADNLVAKKCEMEF-- 386

QY 383 NTRVQDT---DWKELY--RK-----RHQKESPKGRFVML----- 415
Db 389 NT---QDTGGMCKCIVSDOKXDIVLADKYTCGNVQKPVTOGFRMLILIVHSLLCQY 445
QY 416 -----PSTHTIPFYNPPLPRFPSS 437
Db 446 ITTGLSLMVLVLDVQDAPAGIHFDCTITPLPVPQPLPS 487

RESULT 9

Q9ZUB9 PRELIMINARY; PRT; 350 AA.

AC Q9ZUB9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE F508.32 protein.
GN Name=F508.32;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702;

RP SEQUENCE FROM N.A.
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Iau S., Lenz C.,
RA Li J., Kremeschaia I., Luros J., Altafi H., Gonzalez A., Araujo R.,
RA Buehler E., Conn L., Conway A.B., Dunn P., Hansen N., Hutzar L.,
RA Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W.,
RA Ecker J.R., Federspiel N.A., Theologis A.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [1]

RP SEQUENCE FROM N.A.
RA Theologis;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005990; AAC98032.1; -
DR PIR; H86371; H86371.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR008945; Skp1_Skp2.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS50888; HLH; 1.
KM SEQUENCE 350 AA; 39953 MW; CD0B4C679167446 CRC64;

Query Match 6.8%; Score 187.5; DB 2; Length 350;
Best Local Similarity 24.4%; Pred. No. 0.00022;
Matches 90; Conservative 58; Mismatches 118; Indels 103; Gaps 17;

QY 172 SESVSGQVPHSLR-----TLVSACSDANDLIVLHLMLESGYI 213
Db 22 NSGIEGVPYMDVELAAKSKRLSEPFELKNVLEKSGTSDLT-ALASVHAVMLESGFV 80
QY 214 --PGTE-----AKALSMPEKMKLSGVYKLQYMP-----LCEGSSATLTCPVLGNLIVNATL 265
Db 81 LDRSGDKSPFKSLLSVGRYTLPELITRKQNTV---ESVTVAFQVIGRLVYVGTG 137
QY 266 ---KINNEIRSVKRLQILPESFICKEL--GENVANIYKDLQSLSPFQDLVYPLLA 318
Db 266 ---KINNEIRSVKRLQILPESFICKEL--GENVANIYKDLQSLSPFQDLVYPLLA 318
QY 138 GSKCRVH--MTSLDKRFLPVIDLVDTLKEKQSSSYEVEFLMWVDELVTPLL 194
Db 138 GSKCRVH--MTSLDKRFLPVIDLVDTLKEKQSSSYEVEFLMWVDELVTPLL 194
QY 319 FTRQALNLPDVG-----LVVLPLELKLRIPLRLDVASVLSLAVCRDLFTASNDPLM 372
Db 319 FTRQALNLPDVG-----LVVLPLELKLRIPLRLDVASVLSLAVCRDLFTASNDPLM 372
QY 195 -----IGLCKAGLESPPCLMLPLELKLRIPLRLDVASVLSLAVCRDLFTASNDPLM 429
Db 373 RFLYLIRFRDNTVAVQ--DTEWKELY---RKR--HIQKESPKGRFVMLPSSTHTIP 423
QY 250 EHKCLEEGKGLMKLYTGDVWKRFASFWRKRLDLARNPPIKK----- 296
Db 424 FIPNPLHPPFPSSRLPFIIGEDQRTPLPYVGDPISSLLPGGEIPSPQFPL----- 478
QY 297 --SNRFPPLFPDR-----DRKEPDRFG-----PSDYRFRGLRDP 331
Db 297 --SNRFPPLFPDR-----DRKEPDRFG-----PSDYRFRGLRDP 331

QY 479 RPRFDPVGP 487
 Db 332 RDRFGPRDP 340

RESULT 10
 PSFL DROME STANDARD; PRT; 270 AA.
 AC Q9Y637;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Putative proteasome inhibitor.
 GN ORFNames=CG8979;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Berens P.V., Bernan B.P., Bhandari D., Bolintsov S.,
 RA Borokva D., Botchan M.R., Bouck Y., Brockstein P., Brotler P.,
 RA Burris K.C., Cawley D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Dahike C., Davenport L.B., Davies P.,
 RA de Palcos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabriellian A.Z., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glocker A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hestlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshireit A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sider-Kamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.C.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "the genome sequence of Drosophila melanogaster";
 RL Science 287:12185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley; tissue=Head;
 RX MEDLINE=2426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brockstein P., Yu C., Champe M.,
 RA George R.A., Guerin H., Krommiller B., Paclebo J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celinker S.E.;
 RT "A Drosophila full-length cDNA resource";
 CC Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -1- FUNCTION: Could play an important role in control of proteasome
 function. Inhibits the hydrolysis of protein and peptide
 substrates by the 20S proteasome (by similarity).

CC -1- SIMILARITY: Belongs to the proteasome inhibitor p131 family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; AE003824; AAM68701.1; -
 CC EMBL; AY058250; AAL13479.1; -
 CC Intact; Q9Y637; -
 CC DR Flybase; Fggn0033669; CG8979.
 CC KW Hypothetical protein; Proteasome.
 CC DOMAIN 169 270 Pro-rich.
 CC SQ SEQUENCE 270 AA; 3008 MW; F7972E7634B90555 CRC64;
 CC
 CC Query Match 5.3%; Score 147; DB 1; Length 270;
 CC Best Local Similarity 21.4%; Pred. No. 0.07;
 CC Matches 83; Conservative 43; Mismatches 90; Indels 172; Gaps 21;
 CC
 CC QY 172 SSSVGGQPHSLSTLYGOS-ADCSNADALVLIHLML-----ESGIYP-QG 216
 CC Db 5 STAKTGDFPYGNDLLYKTVKADVSKSDLLALVHFLTKHYNFRGVGSDKTLPEEG 64
 CC QY 217 TEAKALSPMEKVKLSGV-YKLQYMAP-----LCBSSATLTCVPLGNLIYVNA TLK 266
 CC Db 65 SSL-----LPDSNDDDTKXSLRYVDKMLYLLGHITGSL-----LIMLDLN-TRK 112
 CC QY 267 INNRKSYKRLQLPESFICKEKLGENVANYKIQKSLRFKQOLVPLLA-----FTR 321
 CC Db 113 VSN-----LCVEBELTVPEVKG--ITTIMPSASEIVESYRRLLDPVFTGNSREYTT 163
 CC QY 322 QALNPVDVGLVAVLDELKRTFRLLDVRSVLSLSAVCRDFTASNDPLMRFLRFR 381
 CC Db 164 QTTNSPRRIG-----SPDPL----- 179
 CC QY 382 DNTVAVQDTMKELVKRKHIOKESPK--GRFVMLPSTHTTIPYPNLPFRPPSSRL 439
 CC Db 180 -----RIGEPRRGSEFI-----PSAFSPRRPGF--- 202
 CC QY 440 PGGIIIGGYD-----QRPLTPVQDPISLIGPGETSQQPPLPRPVPVPL 488
 CC Db 203 -PDVVRGGLDPLRGCHGNLFSFSPRPNG-----PGP-----VPRDPFNPPL 244
 CC QY 489 FGPNDILPGRGGPNDRFPFRPSRGPRPTD 516
 CC Db 245 ---NNRRGGQGIN-----PDHMRPPD 263
 CC
 CC RESULT 11
 CC Q9Y593 PRELIMINARY; PRT; 434 AA.
 CC AC Q9Y593;
 CC DT 01-NOV-1999 (TREMELREL. 12, Created)
 CC DT 01-NOV-1999 (TREMELREL. 12, Last sequence update)
 CC DT 01-MAR-2004 (TREMELREL. 26, Last annotation update)
 CC DE NY-REN-57 antigen (Fragment).
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC CX NCBI_TaxID=9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=99438124; PubMed=10508479;
 CC RA Scallan M.J., Jordan A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
 CC RA Jongeneel V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
 CC RA Old L.J.;
 CC RT "Antigens recognized by autologous antibody in patients with renal-
 CC cell carcinoma";
 CC RL Int. J.Cancer 83:456-464(1999).
 CC DR EMBL; AF15114; AAD42880.1; -

DR InterPro; IPR001810; F-box.
 DR InterPro; IPR005941; IPR-like.
 DR Pfam; PF00646; F-box; 1.
 DR PROSITE; PS50181; FBOX; 1.
 FT NON TER 1
 SQ SEQUENCE 434 AA; 48863 MM; CF2A074E8371120D CRC64;

Query Match 5.3%; Score 145.5; DB 2; Length 434;
 Best Local Similarity 21.7%; Pred. No. 0.19; Indels 169; Gaps 24;
 Matches 98; Conservative 61; Mismatches 123; Indels 169; Gaps 24;

QY 105 SLATSSNQTSMODEPSPDSFGQAAGSVNDDSMLG-PSQNFPAESIQDNAMAGTGF 163
 DB 75 SSAETGRSRHPDQHPSS--GGRCGGTSPSSAAGRPA5MAEAE--EDCH----- 122
 QY 164 YPSEPMLCSEYEGVPHSLFTLYQSADCSANDALIVLHLMLESGYIPQGTAKA-L 222
 DB 123 -----SDTVR-----ADDEENSS-----PAETDLOAQL 146
 QY 223 SMPEKWLKSGYKLYQYHPLCEG--SSATLTGVPV---GNLIYVNTLTKINNE----- 270
 DB 147 QM-----FRQWMEFLAPGVSSSNLENRPGRARGSLQKTSADTKGQOAKEKA 197
 QY 271 ---IRSV-----KRIQLPE---SFICEKLGENVANYI---KDLQ 302
 DB 198 RELFLKAVEEONGALYEAIKFYRRAMQVDFIEFKITTYRSPDGDGVNSYIEDNDD 257
 QY 303 KLSRL--FKDQLYPPLAFTROALNL--PVV---FGVLVPLELKLRIEFL-----LD 348
 DB 258 KWADLLSYFOOQ-----LTFOESVYKLCQPELESQIHISVLPMEVLYIFRWVSSDLD 312
 QY 349 VRSVLSISAVGRDLFTASNDPLMRFLYLRDFRDNVYR-VQDTWKELRYKRHIQRKSP 407
 DB 313 LRSLEQSLVCGRGFYTCARDEPIWRLACLKVGWGSCTKLVPYTSWREMFLEP-----P 365
 QY 408 KGRFVMLPSSST-----HTIPFPNLPDRPPSSRLPPGIIGGEYDQ 450
 DB 366 RVRFPGVYISKTYTIRQEGSLDGFYRAMHQVEYV---RYIRFPDGHV----- 411
 QY 451 RPTLPYVGDPISSLIIPGGETPSOPPLRPR 481
 DB 412 -----MLTTEEPQSIIVPRLTR 430

RESULT 12

Q9NT57 PRELIMINARY; PRT; 547 AA.
 ID Q9NT57;
 AC Q9NT57;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp43C0118 (Fragment).
 GN Name=DKFZp43C0118;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Outenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AL137520; CAB70786.1; -
 DR PIR; T46366; T46366;
 DR InterPro; IPR001810; F-box.
 DR pfam; PF00646; F-box; 1.
 DR PROSITE; PS50181; FBOX; 1.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 547 AA; 62217 MM; A726E8315A82DF31 CRC64;

Query Match 5.3%; Score 145.5; DB 2; Length 547;

Best Local Similarity 21.7%; Pred. No. 0.26;
 Matches 98; Conservative 61; Mismatches 123; Indels 169; Gaps 24;

QY 105 SLATSSNQTSMODEPSPDSFGQAAGSVNDDSMLG-PSQNFPAESIQDNAMAGTGF 163
 DB 72 SSAETGRSRHPDQHPSS--GGRCGGTSPSSAAGRPA5MAEAE--EDCH----- 119
 QY 164 YPSEPMLCSEYEGVPHSLFTLYQSADCSANDALIVLHLMLESGYIPQGTAKA-L 222
 DB 120 -----SDTVR-----ADDEENSS-----PAETDLOAQL 143
 QY 223 SMPEKWLKSGYKLYQYHPLCEG--SSATLTGVPV---GNLIYVNTLTKINNE----- 270
 DB 144 QM-----FRQWMEFLAPGVSSSNLENRPGRARGSLQKTSADTKGQOAKEKA 194
 QY 271 ---IRSV-----KRIQLPE---SFICEKLGENVANYI---KDLQ 302
 DB 198 RELFLKAVEEONGALYEAIKFYRRAMQVDFIEFKITTYRSPDGDGVNSYIEDNDD 254
 QY 303 KLSRL--FKDQLYPPLAFTROALNL--PVV---FGVLVPLELKLRIEFL-----LD 348
 DB 258 KWADLLSYFOOQ-----LTFOESVYKLCQPELESQIHISVLPMEVLYIFRWVSSDLD 309
 QY 349 VRSVLSISAVGRDLFTASNDPLMRFLYLRDFRDNVYR-VQDTWKELRYKRHIQRKSP 407
 DB 310 LRSLEQSLVCGRGFYTCARDEPIWRLACLKVGWGSCTKLVPYTSWREMFLEP-----P 362
 QY 408 KGRFVMLPSSST-----HTIPFPNLPDRPPSSRLPPGIIGGEYDQ 450
 DB 366 RVRFPGVYISKTYTIRQEGSLDGFYRAMHQVEYV---RYIRFPDGHV----- 408
 QY 451 RPTLPYVGDPISSLIIPGGETPSOPPLRPR 481
 DB 409 -----MLTTEEPQSIIVPRLTR 427

RESULT 13

Q6PKH7 PRELIMINARY; PRT; 403 AA.
 ID Q6PKH7;
 AC Q6PKH7;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE FBXO9 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Shapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Vallalath D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Small D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC000650; AAH00650.2;
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR008941; TPR-like.
 DR Pfam; PF00646; F-box; 1.
 DR PROSITE; PS0181; FBOX; 1.
 SQ SEQUENCE 403 AA; 47361 MW; 1AAALF46C31315SB CRC64;

Query Match 5.2%; Score 144; DB 2; Length 403;
 Best Local Similarity 23.1%; Pred. No. 0.21;
 Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;

QY 233 VYKIQVMEPLCEG--SSATLTVCPL-----GNLIVNATLKINNE-----IRSV-- 274
 DB 1 MFRQWMFELAPGVSSNLENRPGRARGSLQKTSADTKGQOAKEKARELFLKAVEE 60
 QY 275 -----KRLQLPPE-----SFICKKLGENVANYI---KDLOKLSRL---FK 309
 DB 61 EONGALYEAIKFYRRAMQVLVDIEFKITTRSPDGGVGNSTYEDNDSDSKMADLSYFQ 120
 QY 310 DQLYVPLAFTROALNL--PDV---FGLVVLPLELKLRIPL-----LDVRSVLSLAV 358
 DB 121 QQ-----LTFQESVYLKCOPELESQIHISVLEMEVLMIYFRWVSSDLDRSLQSLIV 175
 QY 359 CRDLFTASNDPLMFLRFLYLRDPFRONTVR-VODTWMKELRYKRHIQRKSPKGFVLLPS 417
 DB 176 CREGYICARDEIWRKLACIKWGRSCIKLVPTYSKREFLER-----PVRFPDGVYIS 228
 QY 418 ST-----HTIPFPNPLHPRFPSSRLPGIIGGEYDQRPFLPYVGD 460
 DB 229 KTTYIROGEGSLDGFYRAMHQVEY--RYIRFPDGHV----- 264
 QY 461 ISSLIIPGGETPSQFPPLRPR 481
 DB 265 --WMLTPEEPOSTIVPRLRTR 283

RESULT 14
 AAH00650 PRELIMINARY; PRT; 403 AA.
 AC AAH00650;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE FBOX9 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusita K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toobyki S., Canninci P., Prange C.,
 RA Raha S.S., Loezliano N.A., Peters G.J., Abramson R.D., Mulvey S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Woley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettelman M., Nadeau A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC000650; AAH00650.2;
 SQ SEQUENCE 403 AA; 47361 MW; 1AAALF46C31315SB CRC64;

Query Match 5.2%; Score 144; DB 2; Length 403;
 Best Local Similarity 23.1%; Pred. No. 0.21;
 Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;

QY 233 VYKIQVMEPLCEG--SSATLTVCPL-----GNLIVNATLKINNE-----IRSV-- 274
 DB 1 MFRQWMFELAPGVSSNLENRPGRARGSLQKTSADTKGQOAKEKARELFLKAVEE 60
 QY 275 -----KRLQLPPE-----SFICKKLGENVANYI---KDLOKLSRL---FK 309
 DB 61 EONGALYEAIKFYRRAMQVLVDIEFKITTRSPDGGVGNSTYEDNDSDSKMADLSYFQ 120
 QY 310 DQLYVPLAFTROALNL--PDV---FGLVVLPLELKLRIPL-----LDVRSVLSLAV 358
 DB 121 QQ-----LTFQESVYLKCOPELESQIHISVLEMEVLMIYFRWVSSDLDRSLQSLIV 175
 QY 359 CRDLFTASNDPLMFLRFLYLRDPFRONTVR-VODTWMKELRYKRHIQRKSPKGFVLLPS 417
 DB 176 CREGYICARDEIWRKLACIKWGRSCIKLVPTYSKREFLER-----PVRFPDGVYIS 228
 QY 418 ST-----HTIPFPNPLHPRFPSSRLPGIIGGEYDQRPFLPYVGD 460
 DB 229 KTTYIROGEGSLDGFYRAMHQVEY--RYIRFPDGHV----- 264
 QY 461 ISSLIIPGGETPSQFPPLRPR 481
 DB 265 --WMLTPEEPOSTIVPRLRTR 283

RESULT 15
 FBX9_HUMAN STANDARD; PRT; 447 AA.
 ID FBX9_HUMAN
 AC Q9UK97; O75986;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 01-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE F-box only protein 9.
 GN Name=FBX9; Synonyms=FBX9;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
 RA Munnell A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
 RA Whiting L., Jones M.C., Horton K., Hunt S.E., Scott C.E.,
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
 RA Babage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,
 RA Barlow K.P., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
 RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
 RA Bluford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
 RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Copley V.,
 RA Collier R.E., Collins J.E., Colman L.K., Cotby N.R., Coville G.J.,
 RA Culley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,

```

Db      105 EONGALVEAIKRYRRAMOLVDIEFKIYVTRSPGGDGGNSYIEDNDDBDSKMDLSYFQ 154
QY      310 DOLVYELAFTRQALNL--PDY----FGLVYLPELKLKFEFL-----LVRASVLSIAV 358
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      165 QC-----LTFQSVYKTLQGPBELSQIHISVLEHVMYIFRWVYSSDLDRSLQSLV 219
QY      359 CRDLFTASNDPLMFVLYLRFDRTVR-VODTWKELYRRRIQRKESPKGRFVLLPS 417
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      220 CRGFYICADPEIMWLACIKWGRSCILVYTWREMFLEF-----BRVRDGYIS 272
QY      418 ST-----HTLPFNDLHRPPSSLRPLGIGSEYDQRPFLVYGD 460
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      273 KTTYIRQGEQSLDGYRYRMOVEY---RYIRFFPDGHV----- 308
QY      461 ISSLIPGGETPSQEPPLR 481
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      309 --MLTTPPEQSIVRLRTR 327

Search completed: November 16, 2004, 07:12:30
Job time : 206 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 06:55:18 ; Search time 154 Seconds
(without alignments)
1215.953 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLRVRLKRTWPLEVFEETE.....DRPPFRPSRGRPTDRLSFM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729293 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

- Database : A_Geneseq_23Sep04:*
- 1: geneseqp1980s:*
 - 2: geneseqp1990s:*
 - 3: geneseqp2000s:*
 - 4: geneseqp2001s:*
 - 5: geneseqp2002s:*
 - 6: geneseqp2003as:*
 - 7: geneseqp2003bs:*
 - 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2748	99.8	522	6	ADA57283 Human sec
2	2748	99.8	522	6	ADA41163 Human sec
3	2748	99.8	522	6	ABR47958 Human sec
4	2748	99.8	522	7	ADCT4366 Human sec
5	2744	99.6	522	4	AAAB3161 Human SKP
6	2510	91.1	591	2	AAW68521 Human RIP
7	2489	90.4	482	3	AAV83047 F-box piro
8	2489	90.4	482	5	AAO22452 Human F-b
9	2448.5	88.9	607	4	AAU32109 Novel hum
10	2404	87.3	462	5	ABB90109 Human pol
11	2404	87.3	462	6	ADA57586 Human sec
12	2404	87.3	462	6	ADA41482 Human sec
13	2404	87.3	462	6	ABR48139 Human sec
14	2404	87.3	462	7	ADCT4596 Human sec
15	2270	82.4	443	4	AAAB35160 Human SKP
16	2086.5	75.8	549	4	ABG18510 Novel hum
17	1527	55.4	317	5	ABB90108 Human pol
18	1238	45.0	231	7	ADU68946 Human hea
19	1086	39.4	221	6	ADA54155 Human piro
20	714	25.9	174	6	ADA57587 Human sec
21	714	25.9	174	6	ADA41483 Human sec
22	714	25.9	174	6	ABR48140 Human sec
23	714	25.9	174	7	ADCT4597 Human sec
24	714	25.9	175	2	AAV41397 Human sec
25	502	18.2	94	4	AAU32107 Novel hum

26	396	14.4	76	8	ABO54274 Human gen
27	299	10.9	113	3	AAV87356 Human sig
28	265.5	9.6	225	4	ABO06838 Novel hum
29	264.5	9.6	53	4	ABG18509 Novel hum
30	264.5	9.6	53	4	AAU32108 Novel hum
31	249	9.0	47	8	ABO59862 Human gen
32	240.5	8.7	475	3	AAAG29404 Arabidops
33	194	7.0	39	3	AAV83054 F-box mot
34	194	7.0	39	5	AAO22459 Human F-b
35	189	6.9	38	2	AAV02272 A F-box p
36	189	6.9	38	4	AAE08044 Human F-b
37	189	6.9	38	7	AAE39652 Human F-b
38	164	6.0	38	2	AAV02273 A F-box p
39	164	6.0	38	4	AAE08045 Mouse F-b
40	164	6.0	38	7	AAE39653 Mouse F-b
41	152.5	5.5	336	3	AAAG29406 Arabidops
42	152.5	5.5	342	3	AAAG29405 Arabidops
43	147	5.3	270	4	ABR64135 Drosophil
44	145.5	5.3	430	4	AAV41539 Human pol
45	144	5.2	321	3	AAV92341 Human can

ALIGNMENTS

RESULT 1	ADA57283	ADA57283 standard; protein; 522 AA.
ID	ADA57283;	
XX		
AC	ADA57283;	
XX		
DT	20-NOV-2003 (first entry)	
XX		
DE	Human secreted protein #566.	
XX		
KW	Immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;	AbO54274 Human gen
KW	Cytostatic; cerebroprotective; neuroprotective; neurotropic;	AAV87356 Human sig
KW	Cardiovascular; antiarteriosclerotic; gene therapy;	ABO06838 Novel hum
KW	human secreted protein; cancer; CNS disorder; neurodegenerative disorders;	ABG18509 Novel hum
KW	respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;	AAU32108 Novel hum
KW	inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;	ABO59862 Human gen
KW	multiple sclerosis; ischaemic brain injury; Parkinson's disease;	AAAG29404 Arabidops
KW	Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;	AAV83054 F-box mot
KW	triple helix formation; antisense gene therapy; forensic biology.	AAO22459 Human F-b
XX		
OS	Homo sapiens.	AAV02272 A F-box p
XX		AAE08044 Human F-b
PN	WO2002102994-A2.	AAE39652 Human F-b
XX		AAV02273 A F-box p
PD	27-DEC-2002.	AAE08045 Mouse F-b
XX		AAE39653 Mouse F-b
PF	19-MAR-2002; 2002NO-US008278.	AAAG29406 Arabidops
XX		AAAG29405 Arabidops
PR	21-MAR-2001; 2001US-0277340P.	ABR64135 Drosophil
PR	19-JUL-2001; 2001US-0306171P.	AAV41539 Human pol
PR	13-NOV-2001; 2001US-0331287P.	AAV92341 Human can
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Ruben SM;	
XX		
DR	WPI; 2003-167512/16.	
DR	N-PSDB; ADA56387.	
XX		
PT	New human secreted polypeptides and polynucleotides, useful for	
PT	diagnosing, treating or preventing e.g. immune disorders, inflammatory	
PT	conditions, respiratory disorders, cancers, CNS disorders, or	
XX	neurodegenerative disorders.	
PS	Claim 13; SEQ ID NO 1473; 1754dp; English.	
XX		
CC	The invention relates to 592 new human secreted polypeptides useful for	
CC	diagnosing, treating or preventing e.g. immune disorders, inflammatory	

Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MLRLVRLKRTWPEVETPTGLRSHRLSLCTGWGSSNTRFTITLNYKPLTGE 60
D 1 MLRLVRLKRTWPEVETPTGLRSHRLSLCTGWGSSNTRFTITLNYKPLTGE 60
QY 61 ETLASVIGVSGDILICLLIQQDIPAPNIPSSSTDESHSLQNNQEPPLATSSNQTSMQDEP 120
D 61 ETLASVIGVSGDILICLLIQQDIPAPNIPSSSTDESHSLQNNQEPPLATSSNQTSMQDEP 120
QY 121 SDFSGQAAGSGVWMDSMLGPSQNFPAESIQDNNAHMEGTGFPSBPMLCSESVEGQVP 180
D 121 SDFSGQAAGSGVWMDSMLGPSQNFPAESIQDNNAHMEGTGFPSBPMLCSESVEGQVP 180
QY 181 HSLETLVQSADCSNDALIVLHLLMLESGYIPQGTAKALSMPEKMLSGVYKLQYMH 240
D 181 HSLETLVQSADCSNDALIVLHLLMLESGYIPQGTAKALSMPEKMLSGVYKLQYMH 240
QY 241 PLCEGSSATLTCPVLGNLIVNATLKINNEIRSVKRLQLPESFTCKEKGENVANITYD 300
D 241 PLCEGSSATLTCPVLGNLIVNATLKINNEIRSVKRLQLPESFTCKEKGENVANITYD 300
QY 301 LQKLSRLFKDQVYPLAFTROALNLPDVFGVVLPELKLRIFFLLDVRSVLSAVCR 360
D 301 LQKLSRLFKDQVYPLAFTROALNLPDVFGVVLPELKLRIFFLLDVRSVLSAVCR 360
QY 361 DLFTASNDPLMRFLYLDPRDNTVRVQDTMKELYKRHIQKESPKGRFVWLPSSTH 420
D 361 DLFTASNDPLMRFLYLDPRDNTVRVQDTMKELYKRHIQKESPKGRFVWLPSSTH 420
QY 421 TIIFYPNPLHRRPPSSRLPPGIIGEXYDQRTLPYVGDILISLLIPGGETPSQPPPLRP 480
D 421 TIIFYPNPLHRRPPSSRLPPGIIGEXYDQRTLPYVGDILISLLIPGGETPSQPPPLRP 480
QY 481 RFDVPGPLPGPNPILPGRGPNDRPFRPSRGRPTDGLSLFM 522
D 481 RFDVPGPLPGPNPILPGRGPNDRPFRPSRGRPTDGLSLFM 522
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RESULT 3
ABR47958
ID ABR47958 standard; protein; 522 AA.

AC ABR47958;

DT 12-JUN-2003 (first entry)

DE Human secreted protein, SEQ ID 849.

KM Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
KM vulnerability; antiinflammatory; neuroprotective;
KM antiparkinsonian; gene therapy; human; cardiovascular disorder.

OS Homo sapiens.

XX MO200295010-A2.

PD 28-NOV-2002.

PF 19-MAR-2002; 2002WO-US009785.

PR 21-MAR-2001; 2001US-027734OP.

PR 19-JUL-2001; 2001US-0306171P.

PR 13-NOV-2001; 2001US-031287P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

DR WPI; 2003-129429/12.

PT Novel human secreted proteins, useful for detecting, preventing,
diagnosing, prognosticating, treating and/or ameliorating cardiovascular

PT disorders such as arrhythmia.
XX Claim 13; SEQ ID NO 849; 1881pp; English.

XX The present invention relates to novel human secreted proteins (ABR47953-
XX ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
XX and their coding sequences are useful for the preparation of a diagnostic
XX or pharmaceutical composition for diagnosing or treating a cardiovascular
XX disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
XX arteriosclerosis and myocardial ischemia), neural disorders, immune
XX system disorders, muscular disorders, reproductive disorders,
XX gastrointestinal disorders, pulmonary disorders, renal disorders,
XX proliferative disorders and/or cancerous diseases and conditions, for
XX wound healing and epithelial cell proliferation, to treat inflammation or
XX infection, for treating thrombosis and arteriosclerosis, for treating or
XX preventing neural damage which occurs in neuronal disorders or
XX neurodegenerative conditions such as Alzheimer's disease and Parkinson's
XX disease, to enhance bone and periodontal regeneration and aid in tissue
XX transplants or bone grafts, to prevent skin aging or hair loss, to
XX stimulate growth and differentiation of haematopoietic cells and bone
XX marrow cells when used in combination with other cytokines, to maintain
XX organs before transplantation or for supporting cell culture of primary
XX tissues, to increase or decrease differentiation or proliferation of
XX embryonic stem cells, or to modulate mammalian characteristics or
XX metabolism. Note: The sequence data for this patent was published in
XX electronic format and is available from WIP0 at
XX ftp.wipo.int/pub/published_pct_sequences

Query Match 99.8%; Score 2748; DB 6; Length 522;
Best Local Similarity 99.8%; Pred. No. 5.3e-239;
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MLRLVRLKRTWPEVETPTGLRSHRLSLCTGWGSSNTRFTITLNYKPLTGE 60
D 1 MLRLVRLKRTWPEVETPTGLRSHRLSLCTGWGSSNTRFTITLNYKPLTGE 60
QY 61 ETLASVIGVSGDILICLLIQQDIPAPNIPSSSTDESHSLQNNQEPPLATSSNQTSMQDEP 120
D 61 ETLASVIGVSGDILICLLIQQDIPAPNIPSSSTDESHSLQNNQEPPLATSSNQTSMQDEP 120
QY 121 SDFSGQAAGSGVWMDSMLGPSQNFPAESIQDNNAHMEGTGFPSBPMLCSESVEGQVP 180
D 121 SDFSGQAAGSGVWMDSMLGPSQNFPAESIQDNNAHMEGTGFPSBPMLCSESVEGQVP 180
QY 181 HSLETLVQSADCSNDALIVLHLLMLESGYIPQGTAKALSMPEKMLSGVYKLQYMH 240
D 181 HSLETLVQSADCSNDALIVLHLLMLESGYIPQGTAKALSMPEKMLSGVYKLQYMH 240
QY 241 PLCEGSSATLTCPVLGNLIVNATLKINNEIRSVKRLQLPESFTCKEKGENVANITYD 300
D 241 PLCEGSSATLTCPVLGNLIVNATLKINNEIRSVKRLQLPESFTCKEKGENVANITYD 300
QY 301 LQKLSRLFKDQVYPLAFTROALNLPDVFGVVLPELKLRIFFLLDVRSVLSAVCR 360
D 301 LQKLSRLFKDQVYPLAFTROALNLPDVFGVVLPELKLRIFFLLDVRSVLSAVCR 360
QY 361 DLFTASNDPLMRFLYLDPRDNTVRVQDTMKELYKRHIQKESPKGRFVWLPSSTH 420
D 361 DLFTASNDPLMRFLYLDPRDNTVRVQDTMKELYKRHIQKESPKGRFVWLPSSTH 420
QY 421 TIIFYPNPLHRRPPSSRLPPGIIGEXYDQRTLPYVGDILISLLIPGGETPSQPPPLRP 480
D 421 TIIFYPNPLHRRPPSSRLPPGIIGEXYDQRTLPYVGDILISLLIPGGETPSQPPPLRP 480
QY 481 RFDVPGPLPGPNPILPGRGPNDRPFRPSRGRPTDGLSLFM 522
D 481 RFDVPGPLPGPNPILPGRGPNDRPFRPSRGRPTDGLSLFM 522
```

RESULT 4
ADC74366

ID ADC74366 standard; protein; 522 AA.
XX
AC ADC74366;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted protein - SEQ ID 999.
XX
KW antihaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
KW antidiabetic; immunosuppressive; dermatological; nephrotoxic;
KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virocidic;
KW fungicide; antiparasitic; antiatherosclerotic; vulnerary; cytostatic;
KW haemopoietic; haematologic; anaemia; autoimmune disorder;
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
human.
XX
OS Homo sapiens.
XX
PN MO2003038063-A2.
XX
PD 08-MAY-2003.
XX
PF 19-MAR-2002; 2002WO-US0082277.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-430516/40.
DR N-PSDB; ADC73751.
XX
PT New human secreted polypeptide for diagnosing, preventing or treating
PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
PT atherosclerosis).
XX
PS Claim 16; SEQ ID NO 999; 2272pp; English.
XX
CC The invention relates to a novel human secreted polypeptide comprising a
CC defined sequence given in the specification. The polypeptide, nucleic
CC acid molecule, antibody, agonist or antagonist of the invention may be
CC useful for preparing a composition for diagnosing or treating a
CC haemopoietic or haematologic disorder such as anaemia, autoimmune
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC diabetes, systemic lupus erythematosus or glomerulonephritis,
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC disease, wounds and hyperproliferative disorders including
CC atherosclerosis or cancer as well as bacterial, viral, fungal or
CC parasitic infections. The polypeptide may also be used during gene
CC therapy procedures and for identifying a binding partner by contacting
CC the polypeptide with a binding partner and determining whether the
CC binding partner increases or decreases the activity of the polypeptide.
CC The current sequence is that of the human secreted protein of the
CC invention.
XX
SQ Sequence 522 AA;
XX
Query Match 99.8%; Score 2748; DB 7; Length 522;
Best Local Similarity 99.8%; Pred. No. 5.3e-239;
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRLRRLKRTMPLEVPETETPLGLRSHRLSLCTGWSNNRFTITLNYKPLGDE 60
1 MRLRRLKRTMPLEVPETETPLGLRSHRLSLCTGWSNNRFTITLNYKPLGDE 60
DB 1 MRLRRLKRTMPLEVPETETPLGLRSHRLSLCTGWSNNRFTITLNYKPLGDE 60
QY 61 ETLASVIGSDLLICLLDIDIPAPNIPSSITDSEHSSLNQNNQPSLATSSNQTSMODEQP 120

DB 61 ETLASVIGSDLLICLLDIDIPAPNIPSSITDSEHSSLNQNNQPSLATSSNQTSMODEQP 120
QY 121 SDSFGQAAGSGVWVNDSDMLGPSQNFSAESIQDNAAHAAEGTGYFSPSEMLCSSEVGEQVP 180
DB 121 SDSFGQAAGSGVWVNDSDMLGPSQNFSAESIQDNAAHAAEGTGYFSPSEMLCSSEVGEQVP 180
QY 181 HSLFTLYGADCSNDALIVLHILMESGYIQGTAKALSMPEKXKLSGVYKLYMH 240
DB 181 HSLFTLYGADCSNDALIVLHILMESGYIQGTAKALSMPEKXKLSGVYKLYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLPESFICEKLGENVANYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLPESFICEKLGENVANYKD 300
QY 301 LOKLSRLTKDQVLYPLAFTQALNLPVPGVIVLPLETKIRIRLLDVRVLSLSACR 360
DB 301 LOKLSRLTKDQVLYPLAFTQALNLPVPGVIVLPLETKIRIRLLDVRVLSLSACR 360
QY 361 DLFASNDPLMRFLYLDRFDNTVVRVODTDMKELYRKSHIQKESPKGRFVMLPSSSTH 420
DB 361 DLFASNDPLMRFLYLDRFDNTVVRVODTDMKELYRKSHIQKESPKGRFVMLPSSSTH 420
QY 421 TTPFPNPLHPPFPSSRLPGIIGEDYDQRTLPYVGDPISSLLPGRGETPSQFPPLRP 480
DB 421 TTPFPNPLHPPFPSSRLPGIIGEDYDQRTLPYVGDPISSLLPGRGETPSQFPPLRP 480
QY 481 RFDVPGPLPGPVPILPGRGPPDRPFPSPGRPTDGRLSFM 522
DB 481 RFDVPGPLPGPVPILPGRGPPDRPFPSPGRPTDGRLSFM 522
RESULT 5
AAB35161
ID AAB35161 standard; protein; 522 AA.
XX
AC AAB35161;
XX
DT 09-APR-2001 (first entry)
XX
DE Human Skp1-associated F-box protein-1 SAF-beta SEQ ID NO: 10.
XX
KW Human; protein degradation; slah-mediated degradation protein; SMDP;
KW SCF-complex protein; SCF; slah-1alpha; slah-1 interacting protein; SIP;
KW Skp1-associated F-box protein; SAF-1; SAF-2; SMD; cancer cell division;
KW Skp1-associated destruction-box protein; inflammatory disease.
XX
OS Homo sapiens.
XX
PN MO200007207-A2.
XX
PD 21-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US015873.
XX
PR 11-JUN-1999; 99US-00330517.
XX
PA (BURN-) BURNHAM INST.
XX
PI Reed JC, Matsuzawa S;
XX
DR WPI; 2001-071273/08.
DR N-PSDB; AAC67285.
XX
PT Slah-Mediated Degradation Protein, useful for drug screening, for
PT therapeutic applications and for functional genomics.
XX
PS Claim 15; Page 107-108; 121pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC several slah-mediated degradation proteins and SCF-complex proteins,
CC these are designated Slah-1alpha, Slah-1 interacting protein (SIP),
CC encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skp1-

CC associated F-box protein-1alpha and beta and -2 (SAF-1alpha, SAF-1beta
CC and SAF-2) and Skp1-associated destruction-box protein (SAP). The
CC proteins and their coding sequences are useful in the diagnosis and
CC treatment of cancers, disorders where too little cell division occurs
CC such as bone marrow aplasia, immunodeficiencies and inflammatory
CC diseases including sepsis, fibrosis, arthritis and graft versus host
CC disease
XX

SO Sequence 522 AA;

Query Match 99.6%; Score 2744; DB 4; Length 522;

Best Local Similarity 99.6%; Pred. No. 1.2e-238;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MRLKRLKRTWPEVEETPTGHLRSHRLSLCTWGYSSNTRFTITLVKDPITGDE 60
   |||
Db 1 MRLKRLKRTWPEVEETPTGHLRSHRLSLCTWGYSSNTRFTITLVKDPITGDE 60
QY 61 ETLASVIGSGDILICLLODDIPAPNIPSSSTSESHSLQNNQPSLATSSNQTSMODECP 120
   |||
Db 61 ETLASVIGSGDILICLLODDIPAPNIPSSSTSESHSLQNNQPSLATSSNQTSMODECP 120
QY 121 SDSFQGAAGSVMNDMSMLGPSQNFASISIQDANAHABEGTGYPSFPMLCSSVSGQVP 180
   |||
Db 121 SDSFQGAAGSVMNDMSMLGPSQNFASISIQDANAHABEGTGYPSFPMLCSSVSGQVP 180
QY 181 HSLLETLQASDCSDANDALIVLHLMLESGLYPOGTEAKALSMPEKMLSGYKQLQYMH 240
   |||
Db 181 HSLLETLQASDCSDANDALIVLHLMLESGLYPOGTEAKALSMPEKMLSGYKQLQYMH 240
QY 241 PLCEGSSATLTCVPLNSLVNATLKINNEIRSVKRLQLIPESFICEKLGENVANIKYD 300
   |||
Db 241 PLCEGSSATLTCVPLNSLVNATLKINNEIRSVKRLQLIPESFICEKLGENVANIKYD 300
QY 301 LQKLSRFLPKQQLVPLAFTROALNLPDVGVLVPLELKLRTFRLLDVRSVLSAVCR 360
   |||
Db 301 LQKLSRFLPKQQLVPLAFTROALNLPDVGVLVPLELKLRTFRLLDVRSVLSAVCR 360
QY 361 DLFTASNDPLMRLYLRFDRDNTVRVQDTWKELVYKRAIQRKESPKGRFVMLLPBSTH 420
   |||
Db 361 DLFTASNDPLMRLYLRFDRDNTVRVQDTWKELVYKRAIQRKESPKGRFVMLLPBSTH 420
QY 421 TIIPYNPMLHRPPSSRLPPGIIIGSEYDQRTLPYGGPISSLIIRPGSTPSQFPLRP 480
   |||
Db 421 TIIPYNPMLHRPPSSRLPPGIIIGSEYDQRTLPYGGPISSLIIRPGSTPSQFPLRP 480
QY 481 RFDVGPPLPGNPILPGSGGPNDRFPPRSRGRPTDGLSLFM 522
   |||
Db 481 RFDVGPPLPGNPILPGSGGPNDRFPPRSRGRPTDGLSLFM 522

```

RESULT 6

AAW68521 ID AAW68521 standard; protein; 591 AA.

XX AC AAW68521;

XX DT 25-JAN-1999 (first entry)

XX Human RIP-associated protein.

XX Human; RIP-associated protein; RAP; primer; PCR; amplification; probe;
XX hybridization; death domain; MORT module; ICE-like family process;
XX kinase; TRAF domain; inflammation; cell death; tumour; HIV; infection.

XX Homo sapiens.

XX OS Homo sapiens.

XX MO9841624-A1.

XX PD 24-SEP-1998.

XX PF 19-MAR-1998; 98WO-IL000125.

PR 19-MAR-1997; 97IL-00120485.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Wallach D, Kovalenko A;

XX MPI; 1998-531565/45.

DR N-PSDB; AAW57200.

PT DNA encoding RIP-associated protein (RAP) - useful for, e.g. treatment of
PT tumour cells or HIV-infected cells.

PS Claim 10; Fig 2; 65pp; English.

CC This sequence represent part of a human RIP-associated protein (RAP). The
CC coding sequence was isolated from a B-cell library by a yeast 2-hybrid
CC screen using the RIP protein devoid of its "death domain" as a bait. The
CC screen isolated a clone of about 1.9 kb. Primers were generated based on
CC the sequence and used to PCR amplify probes for screening a colon and
CC heart cDNA library. A further 300 bp of sequence was determined, which
CC was added to the 1.9 kb of sequence from the B-cell library. The encoded
CC protein does not contain a "death domain", MORT module, ICE-like family
CC protease domain, kinase domain, nor TRAF domains. RAP was shown to bind
CC only to RIP and not to TRADD, MORT-1, p35-R, p75-R or WACH. The protein
CC can be used to modulate or mediate RIP modulated/mediated intracellular
CC effects on the inflammation, cell death or cell survival pathways in
CC which RIP is involved, e.g. for treating tumour cells or HIV-infected
CC cells

SO Sequence 591 AA;

Query Match 91.1%; Score 2510; DB 2; Length 591;

Best Local Similarity 99.6%; Pred. No. 2.1e-217;
Matches 479; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```

QY 42 SNTRFTITLVKDPITGDEETLASVIGSGDILICLLODDIPAPNIPSSSTSESHSLQNN 101
   |||
Db 113 SNTRFTITLVKDPITGDEETLASVIGSGDILICLLODDIPAPNIPSSSTSESHSLQNN 172
QY 102 EOPSLATSSNQTSMODECPDSFQGAAGSVMNDMSMLGPSQNFASISIQDANAHABEGT 161
   |||
Db 173 EQ--LATSSNQTSMODECPDSFQGAAGSVMNDMSMLGPSQNFASISIQDANAHABEGT 230
QY 162 GYPSBPMLCSSVSGQVPFHSLETLQASDCSDANDALIVLHLMLESGLYPOGTEAKA 221
   |||
Db 231 GYPSBPMLCSSVSGQVPFHSLETLQASDCSDANDALIVLHLMLESGLYPOGTEAKA 290
QY 222 LMPKMKLSGYKQLQYMHPLCEGSSATLTCVPLNSLVNATLKINNEIRSVKRLQLLP 281
   |||
Db 291 LMPKMKLSGYKQLQYMHPLCEGSSATLTCVPLNSLVNATLKINNEIRSVKRLQLLP 350
QY 282 ESFICEKLGENVANIKYDQLKLSRFLPKQQLVPLAFTROALNLPDVGVLVPLELKL 341
   |||
Db 351 ESFICEKLGENVANIKYDQLKLSRFLPKQQLVPLAFTROALNLPDVGVLVPLELKL 410
QY 342 RIIFRLDVRSVLSAVCGDLFTASNDPLMRLYLRFDRDNTVRVQDTWKELVYKRAI 401
   |||
Db 411 RIIFRLDVRSVLSAVCGDLFTASNDPLMRLYLRFDRDNTVRVQDTWKELVYKRAI 470
QY 402 QRKESPKGRFVMLLPBSTHTIIPYNPMLHRPPSSRLPPGIIIGSEYDQRTLPYGGPI 461
   |||
Db 471 QRKESPKGRFVMLLPBSTHTIIPYNPMLHRPPSSRLPPGIIIGSEYDQRTLPYGGPI 530
QY 462 SSLIPGSGTSPQFPLRPDPVGPLPGNPILPGSGGPNDRFPPRSRGRPTDGLSLF 521
   |||
Db 531 SSLIPGSGTSPQFPLRPDPVGPLPGNPILPGSGGPNDRFPPRSRGRPTDGLSLF 590
QY 522 M 522
   |||
Db 591 M 591

```

RESULT 7

AA83047
ID AA83047 standard; protein; 482 AA.
AC AA83047;
XX
XX
XX 16-AUG-2000 (first entry)
DT
XX
XX
DE F-box protein FBP-7.
XX
XX F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist;
XX proliferative disorder; differentiative disorder; breast cancer;
XX prostate cancer; ovarian cancer; cancer; small cell lung carcinoma;
XX immune disorder; cardiovascular disorder; inflammatory disorder; human.
XX Homo sapiens.
OS
XX MO200012679-A1.
PN
XX 09-MAR-2000.
PD
XX
XX 27-AUG-1999; 99WO-US019560.
PF
XX
XX 28-AUG-1998; 98US-0098355P.
PR 03-FEB-1999; 99US-0118568P.
PR 15-MAR-1999; 99US-0124448P.
XX
XX (UNYNY) UNIV NEW YORK STATE.
PA
XX Chlaure DS, Pagano M, Latres E;
PI
XX MPI; 2000-256635/22.
DR N-PSDB; AA293356.
XX
XX Novel nucleic acid for screening compounds useful for treating
PT proliferative and differentiative disorders such as cancer and immune
PT disorders comprises sequences encoding ubiquitin ligases.
XX
XX Claim 10; Fig 10a; 245pp; English.
PS
XX Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases
CC with F-box motifs (F-box proteins) are useful for diagnosis of
CC proliferative and differentiative related disorders by measuring FBP gene
CC expression. Cells expressing such proteins or their fragments are useful
CC for screening compounds. The compounds are agonists or antagonists, which
CC are useful for treating a proliferative or differentiative disorder in a
CC mammal such as breast, ovarian and prostate cancer, and small cell lung
CC carcinoma and also major opportunistic infections, immune disorders,
CC cardiovascular diseases and inflammatory disorders. FBP protein, analogs,
CC derivatives and their subsequences, anti-FBP antibodies are also useful
CC in diagnosis of the disorders
XX
XX Sequence 482 AA;
SQ
Query Match 90.4%; Score 2489; DB 3; Length 482;
Best Local Similarity 98.1%; Pred. No. 1,26-215;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 42 SNTRETTITLANKDPLTGDEFTLASVGIYSGDLICLITODDIPAPNISTSTDESSSQNN 101
DB 2 SNTRETTITLANKDPLTGDEFTLASVGIYSGDLICLITODDIPAPNISTSTDESSSQNN 61
QY 102 EQPSIATSSNOTSNOEQSPDSFQQAAGSVMNDMSLGFQNEASTIQDNAAVAEGT 161
DB 62 EQPSIATSSNOTSNOEQSPDSFQQAAGSVMNDMSLGFQNEASTIQDNAAVAEGT 121
QY 162 GFYSEEPMLGSESEVGGVPHSLFTLYOSADCSNDNDALIVLHMLMESGYTPOGTAKA 221
DB 122 GFYSEEPMLGSESEVGGVPHSLFTLYOSADCSNDNDALIVLHMLMESGYTPOGTAKA 161
QY 222 LSMPEKMLSGVYKLQYVHPLCESSSATLTCVPLGNLIVVATLKINNEIRSVYRIQLLP 261
DB 182 LSMPEKMLSGVYKLQYVHPLCESSSATLTCVPLGNLIVVATLKINNEIRSVYRIQLLP 241

QY 282 ESFICKKLGENVANIYKDLQSLRFLKDLVYPLAFTROALNLPDVGVLVPLELKL 341
DB 242 ESFICKKLGENVANIYKDLQSLRFLKDLVYPLAFTROALNLPDVGVLVPLELKL 301
QY 342 RIFRLIDVASVLSLAVCRDLFTASNDPLWRFVLYLRDPDRNTYAVQDTMKELVRKHI 401
DB 302 RIFRLIDVASVLSLAVCRDLFTASNDPLWRFVLYLRDPDRNTYAVQDTMKELVRKHI 361
QY 402 QKESPKGRFVMLLBSSHTTIFYPNPLHPPSPSSRLPPGIGEVQORPTLPVGDPI 461
DB 362 QKESPKGRFVMLLBSSHTTIFYPNPLHPPSPSSRLPPGIGEVQORPTLPVGDPI 421
QY 462 SSLIPGGTSPQPLPRLRPDPVGLPQNPILPGRGPNDRPFRPSRGRPTDGRLSF 521
DB 422 SSLIPGGTSPQPLPRLRPDPVGLPQNPILPGRGPNDRPFRPSRGRPTDGRLSF 481
QY 522 M 522
DB 482 M 482
RESULT 8
AA02452
ID AA02452 standard; protein; 482 AA.
XX
XX AA02452;
AC
XX 11-OCT-2002 (first entry)
DT
XX
XX Human F-box protein FBP7 SEQ ID No 14.
DE
XX
XX Cytostatic; immunomodulator; cardiant; antiinflammatory; antimicrobial;
XX proliferative; differentiative disorder; Skp2; F-box protein; cancer;
XX ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer;
XX small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP;
XX inflammatory disorder; lymphoma; major opportunistic infection;
XX certain cardiovascular disease; human.
OS
XX Homo sapiens.
XX
XX WO200255665-A2.
PN
XX 18-JUL-2002.
PD
XX
XX 07-JAN-2002; 2002WO-US000311.
PF
XX
XX 05-JAN-2001; 2001US-0260179P.
PR
XX
XX (UNYNY) UNIV NEW YORK STATE.
PA
XX
XX Pagano M;
PI
XX
XX MPI; 2002-59665/64.
DR N-PSDB; AA41047.
DR
XX
XX Screening compounds for treating proliferative disorders, e.g. breast
PT cancer or prostate cancer, infections or immune disorders, comprises
PT detecting a change in the activity of Skp2 with either p27 or Cks1.
XX
XX
XX Disclosure; Fig 10; 246pp; English.
PS
XX The invention relates to screening compounds useful for the treatment of
CC proliferative or differentiative disorders comprising detecting a change
CC in the activity of Skp2 (F-box protein). The method is useful for
CC screening compounds for the treatment of proliferative or differentiative
CC disorders, particularly cancer. These compounds include small molecules,
CC or compounds or derivatives or analogues of the new ubiquitin ligases.
CC The compounds are useful for treating diseases such as cancer (e.g. breast
CC cancer, prostate cancer or ovarian cancer, lymphoma, small cell
CC lung carcinoma or parathyroid adenomas), major opportunistic infections,
CC immune disorders, certain cardiovascular diseases or inflammatory
CC disorders. This sequence represents an F-box protein (FBP) relating to
CC the invention

XX SQ Sequence 482 AA;
Query Match 90.4%; Score 2489; DB 5; Length 482;
Best Local Similarity 98.1%; Pred. No. 1.2e-215;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 42 SNTREITLTVKCDPLTDEETLASVIGSDLICLIQDIDIPAPNIPSSITDSEHSSIQNN 101
DB 2 SNRFFITLVKCDPLTDEETLASVIGSDLICLIHDIIPPNIPSSITDSEHSSIQNN 61
QY 102 EOPSLATSSNOTSQDQSPDSFQGOAAGVWDDMLPSSQNFEXESIQDNAMAEGR 161
DB 62 EOPSLATSSNOTSIQDQSPDSFQGOAAGVWDDMLPSSQNFEXESIQDNAMAEGR 121
QY 162 GFYSEBMLCSESVESGVPHSLFTLYQSADCSANDALIYLIHILMESGYIPQTEAKA 221
DB 122 GFYSEBMLCSESVESGVPHSLFTLYQSADCSANDALIYLIHILMESGYIPQTEAKA 181
QY 222 LSNPEKMKLSGVYKQYMHPLCEGSSATLTCCVPGNIIYVNAIKINNEIRSVKRLQLLP 281
DB 182 LSNPEKMKLSGVYKQYMHPLCEGSSATLTCCVPGNIIYVNAIKINNEIRSVKRLQLLP 241
QY 282 ESFICKEKLGNNVNIYKDLQKLSRLFKDQLVYPLAFTRQALNPVFGVLVLPLEIKU 341
DB 242 ESFICKEKLGNNVNIYKDLQKLSRLFKDQLVYPLAFTRQALNPVFGVLVLPLEIKU 301
QY 342 RIFELLDVRSVLSAVCRDLFTASNDPLLMLRYLDFPDNTVRVODTDWKELYKRHI 401
DB 302 RIFELLDVRSVLSAVCRDLFTASNDPLLMLRYLDFPDNTVRVODTDWKELYKRHI 361
QY 402 QKRSPPGRFVYMLLPSSSTHTIPFPNPLHRRPFPSSSLPPGIIIGGEYDQRTLPYGDPI 461
DB 362 QKRSPPGRFVYMLLPSSSTHTIPFPNPLHRRPFPSSSLPPGIIIGGEYDQRTLPYGDPI 421
QY 462 SSLLPGGETPSQCPPLRPFRDPVGPLPGPNPLPGHGGPNDRFPFRPSGRPTDRLSP 521
DB 422 SSLLPGGETPSQCPPLRPFRDPVGPLPGPNPLPGHGGPNDRFPFRPSGRPTDRLSP 481
QY 522 M 522
DB 482 M 482
RESULT 9
ID AAU32109 standard; protein; 607 AA.
XX AAU32109;
XX 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #2600.
XX Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX Homo sapiens.
XX WO200179449-A2.
XX 25-OCT-2001.
XX 16-APR-2001; 2001WO-US008656.
XX 18-APR-2000; 2000US-00552929.
XX 26-JAN-2001; 2001US-00770160.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX

DR WPI; 2001-611725/70.
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX Claim 20; Page 556; 765bp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU3304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
XX SQ Sequence 607 AA;
Query Match 88.9%; Score 2448.5; DB 4; Length 607;
Best Local Similarity 90.8%; Pred. No. 7.9e-212;
Matches 481; Conservative 7; Mismatches 33; Indels 9; Gaps 5;
QY 1 MLARVRLKRTPLPEVPEPEPTLGLRSHRLSLICTGYSSNRFITLVKCDPLTDE 60
DB 36 MLARVRLKRTPLPEVPEPEPTLGLRSHRLSLICTGYSSNRFITLVKCDPLTDE 95
QY 61 ETLASVIGSDLICLIQDIDIPAPNIPSSITDSEHSSIQNNQPSLATSSNOTSQDQSP 120
DB 96 ETLASVIGSDLICLIQDIDIPAPNIPSSITDSEHSSIQNNQPSLATSSNOTSQDQSP 155
QY 121 SDSFOGAAGSVWDDMLPSSQNFEXESIQDNAMAEGRGFYSEBMLCSESVESGV 180
DB 156 SDSFOGAAGSVWDDMLPSSQNFEXESIQDNAMAEGRGFYSEBMLCSESVESGV 215
QY 181 HSLETTYQSADCSANDALIYLIHILMESGYIPQTEAKALSMEKMKLSGVYKQYMH 240
DB 216 HSLETTYQSADCSANDALIYLIHILMESGYIPQTEAKALSMEKMKLSGVYKQYMH 275
QY 241 PLCEGSSATLTCCVPGNIIYVNAIKINNEIRSVKRLQLLPESFICKEKLGNNVNIYK 300
DB 276 PLCEGSSATLTCCVPGNIIYVNAIKINNEIRSVKRLQLLPESFICKEKLGNNVNIYK 335
QY 301 LQKLSRLPFDQVLVYPLAFTRQALNPVFGVLVLPLEIKIRIFELLDVRSVLSAVCR 360
DB 336 LQKLSRLPFDQVLVYPLAFTRQALNPVFGVLVLPLEIKIRIFELLDVRSVLSAVCR 395
QY 361 DLFTASNDPLLMLRYLDFPDNTVRVODTDWKELYKRHIQKSPGRFVYMLLPSSSTH 420
DB 396 DLFTASNDPLLMLRYLDFPDNTVRVODTDWKELYKRHIQKSPGRFVYMLLPSSSTH 455
QY 421 TTFPFPNPLHRRPFPSSSLPPGIIIGGEYDQRTLPYGDPISSILPFG-GETPS-QRPP 477
DB 456 TTFPFPNPLHRRPFPSSSLPPGIIIGGEYDQRTLPYGDPISSILPFG-GETPS-QRPP 515
QY 478 -----LRPFDVGPLPGPNPLPGHGGPNDRFPFRPSGRPTDRLSPF 522
DB 516 TETHALNPSPWPPISRDNPQSCPGAEGAPPNRTTRPPPLRPQ-GGRALIM 564
RESULT 10
ID ABB90109 standard; protein; 462 AA.
XX ABB90109
XX ABB90109;
AC ABB90109;

```

XX 24-MAY-2002 (first entry)
DT
XX
XX Human polypeptide SEQ ID NO 2485.
DE
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;
KW vulnerrary; anticovulsant; antibacterial; antifungal; antiparasitic;
KW cardiact; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
XX Homo sapiens.
OS
XX WO200190304-A2.
PN
XX 29-NOV-2001.
PD
XX 18-MAY-2001; 2001WO-US016450.
PF
XX 19-MAY-2000; 2000US-0205515P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Birse CE, Rosen CA;
PI
XX WPI; 2002-122018/16.
XX N-PSDB; ABL90518.
DR
XX
XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders.
XX
XX Claim 11; SEQ ID NO 2485; 2081bp + Sequence listing; English.
XX
XX The invention relates to novel genes (ABL89449-ABL90553) and proteins
CC (AB894040-AB890444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer; and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 462 AA;
SQ
Query Match 87.3%; Score 2404; DB 5; Length 462;
Best Local Similarity 88.1%; Pred. No. 5-5e-208;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

```

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DB 181 HSLFTLYQSADCSANDALIVLHLLMLESGYIPQGTBAKALSMPEKMKLSGVYKQYMH 240
QY 241 PLCEGSSATLTCVPLIGNLIVNATLKINNEIRSVKQLPLPESFLCKELGNNANIKD 300
DB 241 PLCEGSSATLTCVPLIGNLIVN----- 262
QY 301 LQKRLRFQDQVYVPLAFAFRQALNLPVFGVIVVPLELKLRIFFLLDVRSVLSAVCR 360
DB 263 -----ANLPDVFGLVIVPLELKLIRIRLLDVRSVLSAVCR 300
QY 361 DLFASNDPLWRFLYLADFRDNTVRVODTMKELYRRKHIOKESPKGRFVMLIPSSTH 420
DB 301 DLFASNDPLWRFLYLADFRDNTVRVODTMKELYRRKHIOKESPKGRFVMLIPSSTH 360
QY 421 TTFYPNPLHPPFPSSRLPGIIGGEYDQRTLPYVGDPISSLIPGGEPSQPPPLRP 480
DB 361 TTFYPNPLHPPFPSSRLPGIIGGEYDQRTLPYVGDPISSLIPGGEPSQPPPLRP 420
QY 481 RPDVGPPLPGPNILPGRGPNDRPFRPSRGRPTGRLSFM 522
DB 421 RPDVGPPLPGPNILPGRGPNDRPFRPSRGRPTGRLSFM 462

```

RESULT 11

ADA57586
ID ADA57586 standard; protein; 462 AA.

XX
XX ADA57586;
AC
XX 20-NOV-2003 (first entry)
DT
XX Human secreted protein #566.
DE
XX
XX Immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.
XX
XX Homo sapiens.
OS
XX WO2002102994-A2.
PN
XX 27-DEC-2002.
PD
XX 19-MAR-2002; 2002WO-US008278.
PF
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Ruben SM;
PI
XX WPI; 2003-167512/16.
XX N-PSDB; ADA56693.
DR
XX New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX
XX Claim 13; SEQ ID NO 1779; 1754bp; English.
XX
XX The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid

sequence at least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, nucleic acids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune disorders, inflammatory conditions (e.g. inflammatory bowel disease, nephritis or Crohn's disease), respiratory disorders (e.g. asthma and allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative disorders (e.g. Parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The polynucleotides are useful for chromosome identification, chromosome mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and as hybridization probes. The polypeptides are useful for as molecular weight markers on sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels, to raise antibodies, for testing biological activities, and for treating or preventing neural disorders, immune system disorders, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, proliferative and/or cancerous diseases. This sequence corresponds to one of the polypeptide of the invention. Note: The sequence data for in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 462 AA:

Query Match 87.3%; Score 2404; DB 6; Length 462;

Best Local Similarity 88.1%; Pred. No. 5.5e-208; Mismatches 2; Indels 60; Gaps 1;

Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRRLIKRTWPLEVETETETLGRSHRLSLCTWGYSSNTRFTITNAYKDLTGDE 60
 Db 1 MRLRRLIKRTWPLEVETETETLGRSHRLSLCTWGYSSNTRFTITNAYKDLTGDE 60
 QY 61 ETLASVGVSGDILCLIIQDDIPAPNTSSSTFSSHLNNEQSLTSSNOMDEOP 120
 Db 61 ETLASVGVSGDILCLIIQDDIPAPNTSSSTFSSHLNNEQSLTSSNOMDEOP 120
 QY 121 SDSFOGAAGSVMNDSDMLGPSQNFPAESIODNNAHAEGTGFPSHPMLCSSEVEGQVP 180
 Db 121 SDSFOGAAGSVMNDSDMLGPSQNFPAESIODNNAHAEGTGFPSHPMLCSSEVEGQVP 180
 QY 121 SDSFOGAAGSVMNDSDMLGPSQNFPAESIODNNAHAEGTGFPSHPMLCSSEVEGQVP 180
 Db 121 SDSFOGAAGSVMNDSDMLGPSQNFPAESIODNNAHAEGTGFPSHPMLCSSEVEGQVP 180
 QY 181 HSLRTVQASDCSANDALIVLHLMLESGYIPQGTBAKALSPKWKLSGYKQYMH 240
 Db 181 HSLRTVQASDCSANDALIVLHLMLESGYIPQGTBAKALSPKWKLSGYKQYMH 240
 QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVRLLPESFICEKLGENVANTYKD 300
 Db 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVRLLPESFICEKLGENVANTYKD 300
 QY 301 LQKLSRLFKQDLVPLIAFTROALNPDVGVVLPELKIRIFRLIDVRSVLSAVCR 360
 Db 301 LQKLSRLFKQDLVPLIAFTROALNPDVGVVLPELKIRIFRLIDVRSVLSAVCR 360
 QY 361 DLFTASNDPLMLRFLYLRDPNDTVRVODTQWKLKYKRMHQRKESKGFVMLPSSTH 420
 Db 361 DLFTASNDPLMLRFLYLRDPNDTVRVODTQWKLKYKRMHQRKESKGFVMLPSSTH 420
 QY 421 TIFPYPNPLHRPPSSRLPPGIIIGGEYDQFTPLPYVGDPISLIPPGSGTSPQFPPLRP 480
 Db 421 TIFPYPNPLHRPPSSRLPPGIIIGGEYDQFTPLPYVGDPISLIPPGSGTSPQFPPLRP 480
 QY 481 RFDEVGPLPGNPILPGRGNDPFRPSPRGRTDRLSLFM 522
 Db 481 RFDEVGPLPGNPILPGRGNDPFRPSPRGRTDRLSLFM 522
 QY 421 RFDEVGPLPGNPILPGRGNDPFRPSPRGRTDRLSLFM 462
 Db 421 RFDEVGPLPGNPILPGRGNDPFRPSPRGRTDRLSLFM 462

RESULT 12
 ADA41482
 ID ADA41482 standard; protein; 462 AA.
 XX

AC ADA41482;

XX 20-NOV-2003 (first entry)

XX Human secreted protein.

XX Human; secreted protein; cancer; hyperproliferative disorder;

XX Rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;

XX Anaemia; allergic reaction; asthma; cardiovascular disorder;

XX wound healing; cytotoxic; immunosuppressive; nootropic; neuroprotective;

XX antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;

XX vulnery; cardiac; gene therapy.

XX Homo sapiens.

XX WO2002102993-A2.

XX 27-DEC-2002.

XX 19-MAR-2002; 2002WO-US008123.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX MPI; 2003-175228/17.

XX New human secreted proteins and nucleic acid molecules, useful for

XX preparing a diagnostic or pharmaceutical composition for diagnosing,

XX preventing or treating cancer or other hyperproliferative disorder,

XX asthma, allergies or AIDS.

XX Claim 1; SEQ ID NO 1865; 3205bp; English.

XX The invention relates to novel genes ADA39629-ADA40565 and proteins

XX ADA40566-ADA44501 for human secreted proteins, useful for preventing,

XX treating or ameliorating medical conditions e.g. by protein or gene

XX therapy. The polypeptides, nucleic acid molecules, antibodies or their

XX fragments, and agonists or antagonists that bind to the polypeptide are

XX useful for preparing a diagnostic or pharmaceutical composition for

XX diagnosing or treating cancer or other hyperproliferative disorder. The

XX polypeptides and nucleic acid molecules are also useful for detecting,

XX preventing, diagnosing, prognosticating, treating or ameliorating cancer

XX or other hyperproliferative disorders including neoplasms, autoimmune

XX disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus

XX erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic

XX anaemia), haematopoietic or haematological disorders (e.g. anaemia,

XX thrombocytopenia), allergic reactions including asthma or eczema,

XX inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory

XX bowel disease or Crohn's disease), neurodegenerative disorders (e.g.

XX Alzheimer's disease or Parkinson's disease), cardiovascular disorders

XX (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,

XX fungal or viral infections including HIV/AIDS), or wound healing and

XX disorders of epithelial cell proliferation. The nucleic acids are also

XX useful for chromosome identification, radiation hybrid mapping or long-

XX range restriction mapping, as molecular weight markers, or as

XX hybridization or diagnostic probes. The polypeptides and antibodies are

XX useful for providing immunological probes for differential identification

XX of the tissues immunohistochemistry assays. Note: The sequence data for

XX this patent did not form part of the printed specification, but was

XX obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 462 AA;

XX Query Match 87.3%; Score 2404; DB 6; Length 462;

XX Best Local Similarity 88.1%; Pred. No. 5.5e-208;

XX Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLLKRTWPLEVPEPETEPTLGLRSHLSLSLCTGWGYSNTRFTITLNYKDLPTGDE 60
 DB 1 MRLRVLLKRTWPLEVPEPETEPTLGLRSHLSLSLCTGWGYSNTRFTITLNYKDLPTGDE 60
 QY 61 ETLASGYISGDLICLILODDIPAPNIPSSSTDSESSSQNNQPSLATSSNQTSXQDEOP 120
 DB 61 ETLASGYISGDLICLILODDIPAPNIPSSSTDSESSSQNNQPSLATSSNQTSXQDEOP 120
 QY 121 SDSFGQAAGSGVWVNDMSLGPSONFEASIQDNNAHMAEGTFYSEPMLCSESVGEQVP 180
 DB 121 SDSFGQAAGSGVWVNDMSLGPSONFEASIQDNNAHMAEGTFYSEPMLCSESVGEQVP 180
 QY 181 HSLFTLYQSADCSNDALIVLIHLLMESGYIPQGTAKALSMPEKMLSGVYKLOQYM 240
 DB 181 HSLFTLYQSADCSNDALIVLIHLLMESGYIPQGTAKALSMPEKMLSGVYKLOQYM 240
 QY 241 PLCEGSSATLTGCVPLGNLIIVNATLKINNEIRSVRLQLLPSPICKEKLGENVANTYKD 300
 DB 241 PLCEGSSATLTGCVPLGNLIIVNATLKINNEIRSVRLQLLPSPICKEKLGENVANTYKD 300
 QY 301 LQKLSRLFKDQLVYPLAFTROALNLPVFGVLVPLELKLRIPLLDVRSVLSAVCR 360
 DB 301 LQKLSRLFKDQLVYPLAFTROALNLPVFGVLVPLELKLRIPLLDVRSVLSAVCR 360
 QY 361 DLFTASNDPLLMRFYLRLDPRDNTVRVODTWKELYRKRIQRKESKGRFVMLPSSTH 420
 DB 361 DLFTASNDPLLMRFYLRLDPRDNTVRVODTWKELYRKRIQRKESKGRFVMLPSSTH 420
 QY 421 TIFPYNPPLHRRPPSSRLPGIIGGEYDQRTLYVGDPISSLIIPGGETPSQFPPLRP 480
 DB 421 TIFPYNPPLHRRPPSSRLPGIIGGEYDQRTLYVGDPISSLIIPGGETPSQFPPLRP 480
 QY 481 RFDVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
 DB 481 RFDVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
 QY 421 RFDVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 462
 DB 421 RFDVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 462

RESULT 13
 ABR48139 standard; protein; 462 AA.
 ABR48139;
 12-JUN-2003 (first entry)
 Human secreted protein, SEQ ID 1030.
 Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cyostatic;
 vulnerary; antiinflammatory; nootropic; neuroprotective;
 antiparkinsonian; gene therapy; human; cardiovascular disorder.
 Homo sapiens.
 WO200295010-A2.
 28-NOV-2002.
 19-MAR-2002; 2002WO-US009785.
 21-MAR-2001; 2001US-0277340P.
 19-JUL-2001; 2001US-0306171P.
 13-NOV-2001; 2001US-0331287P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Ruben SM;
 WPI; 2003-129429/12.
 Novel human secreted proteins, useful for detecting, preventing,
 PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
 PT disorders such as arrhythmia.

PS Claim 13; SEQ ID NO 1030; 1881bp; English.
 XX
 CC The present invention relates to novel human secreted proteins (ABR47633-
 CC ABR48145) and their coding sequences (ACC050344-ACC050856). The proteins
 CC and their coding sequences are useful for the preparation of a diagnostic
 CC or pharmaceutical composition for diagnosing or treating a cardiovascular
 CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
 CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, renal disorders,
 CC proliferative disorders and/or cancerous diseases and conditions, for
 CC wound healing and epithelial cell proliferation, to treat inflammation or
 CC infection, for treating thrombosis and arteriosclerosis, for treating or
 CC preventing neural damage which occurs in neuronal disorders or
 CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
 CC disease, to enhance bone and periodontal regeneration and aid in tissue
 CC transplants or bone grafts, to prevent skin aging or hair loss, to
 CC stimulate growth and differentiation of haematopoietic cells and bone
 CC marrow cells when used in combination with other cytokines, to maintain
 CC organs before transplantation or for supporting cell culture of primary
 CC tissues, to increase or decrease differentiation or proliferation of
 CC embryonic stem cells, or to modulate mammalian characteristics or
 CC metabolism. Note: The sequence data for this patent was published in
 CC electronic format and is available from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 462 AA;
 Query Match 87.3%; Score 2404; DB 6; Length 462;
 Best Local Similarity 88.1%; Pred. No. 5; se=208;
 Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLLKRTWPLEVPEPETEPTLGLRSHLSLSLCTGWGYSNTRFTITLNYKDLPTGDE 60
 DB 1 MRLRVLLKRTWPLEVPEPETEPTLGLRSHLSLSLCTGWGYSNTRFTITLNYKDLPTGDE 60
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 DB 61 ETLASGYISGDLICLILODDIPAPNIPSSSTDSESSSQNNQPSLATSSNQTSXQDEOP 120
 QY 121 SDSFGQAAGSGVWVNDMSLGPSONFEASIQDNNAHMAEGTFYSEPMLCSESVGEQVP 180
 DB 121 SDSFGQAAGSGVWVNDMSLGPSONFEASIQDNNAHMAEGTFYSEPMLCSESVGEQVP 180
 QY 181 HSLFTLYQSADCSNDALIVLIHLLMESGYIPQGTAKALSMPEKMLSGVYKLOQYM 240
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 QY 241 PLCEGSSATLTGCVPLGNLIIVNATLKINNEIRSVRLQLLPSPICKEKLGENVANTYKD 300
 DB 241 PLCEGSSATLTGCVPLGNLIIVNATLKINNEIRSVRLQLLPSPICKEKLGENVANTYKD 300
 QY 301 LQKLSRLFKDQLVYPLAFTROALNLPVFGVLVPLELKLRIPLLDVRSVLSAVCR 360
 DB 301 LQKLSRLFKDQLVYPLAFTROALNLPVFGVLVPLELKLRIPLLDVRSVLSAVCR 360
 QY 361 DLFTASNDPLLMRFYLRLDPRDNTVRVODTWKELYRKRIQRKESKGRFVMLPSSTH 420
 DB 361 DLFTASNDPLLMRFYLRLDPRDNTVRVODTWKELYRKRIQRKESKGRFVMLPSSTH 420
 QY 421 TIFPYNPPLHRRPPSSRLPGIIGGEYDQRTLYVGDPISSLIIPGGETPSQFPPLRP 480
 DB 421 TIFPYNPPLHRRPPSSRLPGIIGGEYDQRTLYVGDPISSLIIPGGETPSQFPPLRP 480
 QY 481 RFDVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
 DB 481 RFDVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
 QY 421 RFDVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 462
 DB 421 RFDVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 462

RESULT 14
 ABR474596 standard; protein; 462 AA.
 ABR474596
 ADCT4596

CC proteins and their coding sequences are useful in the diagnosis and
CC treatment of cancers, disorders where too little cell division occurs
CC such as bone marrow aplasia, immunodeficiencies and inflammatory
CC diseases including sepsis, fibrosis, arthritis and graft versus host
CC disease

XX Sequence 443 AA;

Query Match 82.4%; Score 2270; DB 4; Length 443;
Best Local Similarity 99.8%; Pred. No. 6.7e-196;
Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 92 DSEHSSLQNNQPSLATSSNOTSWQDEQPSFSGQAAGSWNDSDMLGPSQNFEESEI 151
Db 13 DSEHSSLQNNQPSLATSSNOTSWQDEQPSFSGQAAGSWNDSDMLGPSQNFEESEI 72
QY 152 QDNHMAEGTGFYSEPEMLCSSEYEGQVPHSLFTLYOSADCSNDALIVLHILMLESG 211
Db 73 QDNHMAEGTGFYSEPEMLCSSEYEGQVPHSLFTLYOSADCSNDALIVLHILMLESG 132
QY 212 YIPQTEAKALSMPEKWLGSVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEI 271
Db 133 YIPQTEAKALSMPEKWLGSVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEI 192
QY 272 RSVKRLQLLPESFCKEKLGENVANITYKDLQKLSRLFKDQIVYPLAFTQAALNLPVFG 331
Db 193 RSVKRLQLLPESFCKEKLGENVANITYKDLQKLSRLFKDQIVYPLAFTQAALNLPVFG 252
QY 332 LVVLPLEIKLRIPLLDVRSVLSLAVCRDLFTASNDPLMRFYLRDPRDNTYRVQDIT 391
Db 253 LVVLPLEIKLRIPLLDVRSVLSLAVCRDLFTASNDPLMRFYLRDPRDNTYRVQDIT 312
QY 392 WKELYRKPHIQKESPKGRFVMLPSSTHTIPFYPNPLHPPPPSSRLPGIIGGEYDQR 451
Db 313 WKELYRKPHIQKESPKGRFVMLPSSTHTIPFYPNPLHPPPPSSRLPGIIGGEYDQR 372
QY 452 PTLFVYGDPISSLIPGPEIPSQPFPLRPDPVGPLGPNPILPGRGGNDRPPFRPSR 511
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QY 512 GRPTDGRUSFM 522
Db 433 GRPTDGRUSFM 443
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Job time : 159 secs

Tue Nov 16 07:54:47 2004

us-09-927-458-2.rapb

Page 1

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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:09:10 ; Search time 141 Seconds

(without alignments)
1309.884 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 2754

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 35381937 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2754	100.0	522	9	US-09-927-458-2
2	2754	100.0	522	14	US-10-245-593-2
3	2744	99.6	522	16	US-10-679-246-10
4	2489	90.4	482	13	US-10-042-417-14
5	2404	87.3	462	10	US-09-397-945-200
6	2404	87.3	462	15	US-10-264-237-2485
7	2404	87.3	462	15	US-10-653-595-200
8	2404	87.3	497	10	US-09-397-945-435
9	2404	87.3	443	16	US-10-679-246-8
10	2270	82.4	443	16	US-10-264-237-2484
11	1527	55.0	317	15	US-10-408-7654-752
12	1238	45.0	231	16	US-10-408-7654-752
13	1086	39.4	221	14	US-10-094-749-1723

14	714	25.9	174	10	US-09-397-945-434	Sequence 434, App
15	714	25.9	174	15	US-10-653-595-209	Sequence 209, App
16	714	25.9	174	15	US-10-653-595-434	Sequence 434, App
17	714	25.9	175	15	US-09-357-945-209	Sequence 209, App
18	396	14.4	76	14	US-10-029-386-27908	Sequence 27908, A
19	249	9.0	47	14	US-10-029-386-33496	Sequence 33496, A
20	215.5	7.8	500	17	US-10-739-930-9910	Sequence 9910, Ap
21	211	7.7	485	15	US-10-425-114-59910	Sequence 59910, A
22	207	7.5	485	15	US-10-425-114-59911	Sequence 59911, A
23	201	7.3	485	15	US-10-425-114-60984	Sequence 60984, A
24	198	7.2	447	17	US-10-425-115-349540	Sequence 349540, A
25	194	7.0	39	13	US-10-042-417-21	Sequence 21, Appl
26	189	6.9	38	11	US-09-801-348-47	Sequence 47, Appl
27	164	6.0	38	11	US-09-801-348-49	Sequence 49, Appl
28	144	5.2	408	15	US-10-264-237-1835	Sequence 1835, Ap
29	142	5.2	1131	17	US-10-425-115-355048	Sequence 355048, A
30	140	5.1	379	15	US-10-264-049-2807	Sequence 2807, Ap
31	139	5.0	327	13	US-10-042-417-58	Sequence 58, Appl
32	139	5.0	327	16	US-10-679-246-12	Sequence 12, Appl
33	137	5.0	664	16	US-10-437-963-176808	Sequence 176808, A
34	129.5	4.7	197	17	US-10-425-115-356769	Sequence 356769, A
35	126	4.6	344	14	US-10-061-043A-27	Sequence 27, Appl
36	126	4.6	344	14	US-10-060-634C-27	Sequence 27, Appl
37	126	4.6	355	14	US-10-061-043A-35	Sequence 35, Appl
38	126	4.6	355	14	US-10-060-634C-35	Sequence 35, Appl
39	126	4.6	355	14	US-10-094-749-2883	Sequence 2883, Ap
40	125.5	4.6	754	16	US-10-437-963-134895	Sequence 134895, A
41	125	4.5	168	15	US-10-424-599-190794	Sequence 190794, A
42	125	4.5	204	15	US-10-424-599-283065	Sequence 283065, A
43	123	4.5	1827	16	US-10-437-963-158691	Sequence 158691, A
44	120.5	4.4	133	17	US-10-425-115-352606	Sequence 352606, A
45	120	4.4	684	16	US-10-687-732-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-927-458-2
Sequence 2, Application US/09927458
Patent No. US20020058024A1
GENERAL INFORMATION:
APPLICANT: KOVACHENKO, David
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR F
FILE REFERENCE: WALLACH-22A
CURRENT APPLICATION NUMBER: US/09/927,458
CURRENT FILING DATE: 2001-08-13
PRIORITY APPLICATION NUMBER: PCT/IL98/00125
PRIORITY FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: IL 120485
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: 09/381,358
PRIOR FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 522
TYPE: PRT
ORGANISM: Homo sapiens
US-09-927-458-2
Query Match 100.0%; Score 2754; DB 9; Length 522;
Best Local Similarity 100.0%; Pred. No. 4.9e-223;
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLRVLLKRTWPLEVPEPEPTGLRSHRLSLCTGVSNTFRITLTKYKPLTDE 60
Db 1 MRLRVLLKRTWPLEVPEPEPTGLRSHRLSLCTGVSNTFRITLTKYKPLTDE 60
QY 61 ETLAAYGVSDLLILLIODDIPANITSSSTDSHSSQNNQPSLASSNQTGNODECP 120

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Db      61  ETLASGYIVSGDLICILLODDIPAPNIPSSNDSEHSLQNNQPSLATSSNQTSMODEQP 120
Qy      121  SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGFYPSPEMILCSSEVGEQVP 180
Db      121  SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGFYPSPEMILCSSEVGEQVP 180
Qy      181  HSELTIVQSADCSNDALIVLHLMLESQYIPQGTAKALSMPEKMLSGVYKLOVMH 240
Db      181  HSELTIVQSADCSNDALIVLHLMLESQYIPQGTAKALSMPEKMLSGVYKLOVMH 240
Qy      241  PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300
Db      241  PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300
Qy      301  LQKLSRLFKDQVLYPLAFTRQALNLPVFGVLVPLELKRIIRLLDVRSVLSAVCR 360
Db      301  LQKLSRLFKDQVLYPLAFTRQALNLPVFGVLVPLELKRIIRLLDVRSVLSAVCR 360
Qy      361  DLFTASNDPLMLRFLYLDRFDNTVRYVQDTWKELYRKRIQRKESPKGRFVMLPSSSTH 420
Db      361  DLFTASNDPLMLRFLYLDRFDNTVRYVQDTWKELYRKRIQRKESPKGRFVMLPSSSTH 420
Qy      421  TTFYFNPPLHRRPFPSSSLPGIIGGEYDQRPPLPYVGDPISSILPGGEPSPQFPPLRP 480
Db      421  TTFYFNPPLHRRPFPSSSLPGIIGGEYDQRPPLPYVGDPISSILPGGEPSPQFPPLRP 480
Qy      481  RFDYVGPLGPNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
Db      481  RFDYVGPLGPNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522

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RESULT 2
US-10-245-593-2
Sequence 2, Application US/10245593
Publication No. US20030039646A1
GENERAL INFORMATION:

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; APPLICANT: WALLACH, David
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR
; FILE REFERENCE: WALLACH=22A
; CURRENT APPLICATION NUMBER: US/10/245,593
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US/09/927,458
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: PCT/IL98/00125
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: IL 120485
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: 09/381,358
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-593-2

```

Query Match 100.0%; Score 2754; DB 14; Length 522;
Best Local Similarity 100.0%; Pred. No. 4,9e-223;
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MLRLRLKRTWPLEVPEPTPTLGHLSHLSLCTGWGSSNTRFTTLNKKDPLTQDE 60
Db      1  MLRLRLKRTWPLEVPEPTPTLGHLSHLSLCTGWGSSNTRFTTLNKKDPLTQDE 60
Qy      61  ETLASGYIVSGDLICILLODDIPAPNIPSSNDSEHSLQNNQPSLATSSNQTSMODEQP 120
Db      61  ETLASGYIVSGDLICILLODDIPAPNIPSSNDSEHSLQNNQPSLATSSNQTSMODEQP 120
Qy      121  SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGFYPSPEMILCSSEVGEQVP 180

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Db      121  SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGFYPSPEMILCSSEVGEQVP 180
Qy      181  HSELTIVQSADCSNDALIVLHLMLESQYIPQGTAKALSMPEKMLSGVYKLOVMH 240
Db      181  HSELTIVQSADCSNDALIVLHLMLESQYIPQGTAKALSMPEKMLSGVYKLOVMH 240
Qy      241  PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300
Db      241  PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300
Qy      301  LQKLSRLFKDQVLYPLAFTRQALNLPVFGVLVPLELKRIIRLLDVRSVLSAVCR 360
Db      301  LQKLSRLFKDQVLYPLAFTRQALNLPVFGVLVPLELKRIIRLLDVRSVLSAVCR 360
Qy      361  DLFTASNDPLMLRFLYLDRFDNTVRYVQDTWKELYRKRIQRKESPKGRFVMLPSSSTH 420
Db      361  DLFTASNDPLMLRFLYLDRFDNTVRYVQDTWKELYRKRIQRKESPKGRFVMLPSSSTH 420
Qy      421  TTFYFNPPLHRRPFPSSSLPGIIGGEYDQRPPLPYVGDPISSILPGGEPSPQFPPLRP 480
Db      421  TTFYFNPPLHRRPFPSSSLPGIIGGEYDQRPPLPYVGDPISSILPGGEPSPQFPPLRP 480
Qy      481  RFDYVGPLGPNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
Db      481  RFDYVGPLGPNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522

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RESULT 3
US-10-679-246-10
Sequence 10, Application US/10679246
Publication No. US20040163138A1
GENERAL INFORMATION:

```

; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 10
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-10

```

Query Match 99.6%; Score 2744; DB 16; Length 522;
Best Local Similarity 99.6%; Pred. No. 3,4e-222;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1  MLRLRLKRTWPLEVPEPTPTLGHLSHLSLCTGWGSSNTRFTTLNKKDPLTQDE 60
Db      1  MLRLRLKRTWPLEVPEPTPTLGHLSHLSLCTGWGSSNTRFTTLNKKDPLTQDE 60
Qy      61  ETLASGYIVSGDLICILLODDIPAPNIPSSNDSEHSLQNNQPSLATSSNQTSMODEQP 120
Db      61  ETLASGYIVSGDLICILLODDIPAPNIPSSNDSEHSLQNNQPSLATSSNQTSMODEQP 120
Qy      121  SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGFYPSPEMILCSSEVGEQVP 180
Db      121  SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGFYPSPEMILCSSEVGEQVP 180
Qy      181  HSELTIVQSADCSNDALIVLHLMLESQYIPQGTAKALSMPEKMLSGVYKLOVMH 240
Db      181  HSELTIVQSADCSNDALIVLHLMLESQYIPQGTAKALSMPEKMLSGVYKLOVMH 240
Qy      241  PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300
Db      241  PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300

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QY 301 LQKSRFLKQOLVPLLAFTROALNLPDVGVLVPLLELKRIFRLIDVRSVLSAVCR 360
Db 301 LQKSRFLKQOLVPLLAFTROALNLPDVGVLVPLLELKRIFRLIDVRSVLSAVCR 360
QY 361 DLFTASNDPLMLRFLYLRDPNDTVRVQDDMKELYKRRHQRKESPKGFVLLPSSTH 420
Db 361 DLFTASNDPLMLRFLYLRDPNDTVRVQDDMKELYKRRHQRKESPKGFVLLPSSTH 420
QY 421 TIPYPNPLHRPPSSRLRPPGIIIGGEYDQFTLLPYGDPISLIPGGETPSQFPLRP 480
Db 421 TIPYPNPLHRPPSSRLRPPGIIIGGEYDQFTLLPYGDPISLIPGGETPSQFPLRP 480
QY 481 RFDVPGPLPGNPILPGRGPNDRPFRPSRGRPTDRLSPM 522
Db 481 RFDVPGPLPGNPILPGRGPNDRPFRPSRGRPTDRLSPM 522

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RESULT 4
US-10-042-417-14
; Sequence 14, Application US/10042417
; Publication No. US20020123082A1
; GENERAL INFORMATION:
; APPLICANT: Pasano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/10/042,417
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-417-14

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```

Query Match 90.4%; Score 2489; DB 13; Length 482;
Best Local Similarity 98.1%; Pred. No. 9,4e-201;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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QY 42 SNRFTTLNKKDPLTDEETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLONN 101
Db 2 SNRFTTLNKKDPLTDEETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLONN 61
QY 102 EOPSLATSSNOTSQMODQSPDSFQGOAAGSWNDDSMGPPSQNFEAESIODNAHMAEGT 161
Db 62 EOPSLATSSNOTSQMODQSPDSFQGOAAGSWNDDSMGPPSQNFEAESIODNAHMAEGT 121
QY 162 GFYSESEMLCSSEYEGVPHSLFTLYQADCSANDALIVLIHLMLSEGYIPQTEAKA 221
Db 122 GFYSESEMLCSSEYEGVPHSLFTLYQADCSANDALIVLIHLMLSEGYIPQTEAKA 181
QY 222 LSMEXKMLSGVYLQYMHPLCEGSSATLTCVPGNLIYVNAATLKINNRYSVKLQQLP 281
Db 182 LSMEXKMLSGVYLQYMHPLCEGSSATLTCVPGNLIYVNAATLKINNRYSVKLQQLP 241
QY 282 ESFICKRKLGENVANIKYDQKLSRLFKDQLYVPLAFTROALNLPDVGVLVPLLELKR 341
Db 242 ESFICKRKLGENVANIKYDQKLSRLFKDQLYVPLAFTROALNLPDVGVLVPLLELKR 301
QY 342 RIFRLIDVRSVLSAVCRDLFTASNDPLMLRFLYLRDPNDTVRVQDDMKELYKRRH 401
Db 302 RIFRLIDVRSVLSAVCRDLFTASNDPLMLRFLYLRDPNDTVRVQDDMKELYKRRH 361
QY 402 QRKSPSPGRFVLMPLPSSTHTIPFPNPLHRPPSSRLRPPGIIIGGEYDQFTLLPYGDP 461
Db 362 QRKSPSPGRFVLMPLPSSTHTIPFPNPLHRPPSSRLRPPGIIIGGEYDQFTLLPYGDP 421
QY 462 SSLIPGGETPSQFPLRPFRDPVGPLPGNPILPGRGPNDRPFRPSRGRPTDRLSP 521
Db 422 SSLIPGGETPSQFPLRPFRDPVGPLPGNPILPGRGPNDRPFRPSRGRPTDRLSP 481

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QY 522 M 522
Db 482 M 482

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RESULT 5
US-09-397-945-200
; Sequence 200, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT APPLICATION NUMBER: US/09/397,945
; PRIOR APPLICATION NUMBER: 1999-09-17
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-397-945-200

```

```

Query Match 87.3%; Score 2404; DB 10; Length 462;
Best Local Similarity 88.1%; Pred. No. 1.3e-193;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

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QY 1 MLRLVRLKRTPLVPEPETEPTLGLHSLRLSLCTGYSSNRPFTTLNKKDPLTDE 60
Db 1 MLRLVRLKRTPLVPEPETEPTLGLHSLRLSLCTGYSSNRPFTTLNKKDPLTDE 60
QY 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLONNQPSLATSSNOTSQMODQ 120
Db 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLONNQPSLATSSNOTSQMODQ 120
QY 121 SPSFQGOAAGSWNDDSMGPPSQNFEAESIODNAHMAEGTGFYSEBMLCSSEYEGVP 180
Db 121 SPSFQGOAAGSWNDDSMGPPSQNFEAESIODNAHMAEGTGFYSEBMLCSSEYEGVP 180
QY 181 HSLFTLYQADCSANDALIVLIHLMLSEGYIPQTEAKALSMPEKMLSGVYLQYMH 240
Db 181 HSLFTLYQADCSANDALIVLIHLMLSEGYIPQTEAKALSMPEKMLSGVYLQYMH 240

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QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPSEFICKELGENVANIYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVN----- 262
QY 301 LQKLSRLFKQDLVPLAFTROALNPVGVGLVYLPIELKRLIRLLDVSVLSAVCR 360
DB 263 -----ALNLPDVGLVVLPIELKRLIRLLDVSVLSAVCR 300
QY 361 DLFTASNDPLMRFLYLRFDFDNTVRVODTDMKELYRKHIQRKESPKGRFVMLPSSTH 420
DB 301 DLFTASNDPLMRFLYLRFDFDNTVRVODTDMKELYRKHIQRKESPKGRFVMLPSSTH 360
QY 421 TTFYPNPLHRRPPSSRLPGIIGGEYDQPTLPYVGDPISSLIIPGGEFSSQFPPLRP 480
DB 361 TTFYPNPLHRRPPSSRLPGIIGGEYDQPTLPYVGDPISSLIIPGGEFSSQFPPLRP 420
QY 481 RFDVGPPLGPNPILPGRGGPNDRFPFRPSRGRPTDRLSPM 522
DB 421 RFDVGPPLGPNPILPGRGGPNDRFPFRPSRGRPTDRLSPM 462

RESULT 6

US-10-264-237-2485
; Sequence 2485, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Biese et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: Patent In Ver. 3.1
; SEQ ID NO: 2485
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2485

Query Match 87.3%; Score 2404; DB 15; Length 462;
Best Local Similarity 88.1%; Pred. No. 1.3e-193;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRRLKRTWPLEVPEPTETPLGHRSHRLSLCTGYSNTRFTTLNFKDPLTGD 60
DB 1 MRLRRLKRTWPLEVPEPTETPLGHRSHRLSLCTGYSNTRFTTLNFKDPLTGD 60
QY 61 ETLASGYISGDLICLILODDIPAPNIPSTDSSEHSIQNNEQPSLATSSNQTSMODEOP 120
DB 61 ETLASGYISGDLICLILODDIPAPNIPSTDSSEHSIQNNEQPSLATSSNQTSMODEOP 120
QY 121 SPSFGQAAGSVWMDSDMLGSPQNFEEESIQDNNAHMAEGFPPSEPMCLCSSEVEGVP 180
DB 121 SPSFGQAAGSVWMDSDMLGSPQNFEEESIQDNNAHMAEGFPPSEPMCLCSSEVEGVP 180
QY 181 HSLFTLYOSADCSANDALIVLHLLMLSGYIPQTEAKALSMPEKWLSGVYKLOYM 240
DB 181 HSLFTLYOSADCSANDALIVLHLLMLSGYIPQTEAKALSMPEKWLSGVYKLOYM 240
QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPSEFICKELGENVANIYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVN----- 262
QY 301 LQKLSRLFKQDLVPLAFTROALNPVGVGLVYLPIELKRLIRLLDVSVLSAVCR 360

DB 263 -----ALNLPDVGLVVLPIELKRLIRLLDVSVLSAVCR 300
QY 361 DLFTASNDPLMRFLYLRFDFDNTVRVODTDMKELYRKHIQRKESPKGRFVMLPSSTH 420
DB 301 DLFTASNDPLMRFLYLRFDFDNTVRVODTDMKELYRKHIQRKESPKGRFVMLPSSTH 360
QY 421 TTFYPNPLHRRPPSSRLPGIIGGEYDQPTLPYVGDPISSLIIPGGEFSSQFPPLRP 480
DB 361 TTFYPNPLHRRPPSSRLPGIIGGEYDQPTLPYVGDPISSLIIPGGEFSSQFPPLRP 420
QY 481 RFDVGPPLGPNPILPGRGGPNDRFPFRPSRGRPTDRLSPM 522
DB 421 RFDVGPPLGPNPILPGRGGPNDRFPFRPSRGRPTDRLSPM 462

RESULT 7

US-10-653-595-200
; Sequence 200, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1C1
; CURRENT APPLICATION NUMBER: US/10/653,595
; PRIOR FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 200
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-653-595-200

Query Match 87.3%; Score 2404; DB 15; Length 462;
Best Local Similarity 88.1%; Pred. No. 1.3e-193;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRRLKRTWPLEVPEPTETPLGHRSHRLSLCTGYSNTRFTTLNFKDPLTGD 60
DB 1 MRLRRLKRTWPLEVPEPTETPLGHRSHRLSLCTGYSNTRFTTLNFKDPLTGD 60
QY 61 ETLASGYISGDLICLILODDIPAPNIPSTDSSEHSIQNNEQPSLATSSNQTSMODEOP 120
DB 61 ETLASGYISGDLICLILODDIPAPNIPSTDSSEHSIQNNEQPSLATSSNQTSMODEOP 120
QY 121 SPSFGQAAGSVWMDSDMLGSPQNFEEESIQDNNAHMAEGFPPSEPMCLCSSEVEGVP 180

Db 121 SDFQQAAGGVWVNDSDMLGPSQNFENSIQDNAMAEGETGYPSPHMLCSSEVGGVP 180
 QY 181 HSELTLYQSADCSANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGYKLYQYMH 240
 Db 181 HSELTLYQSADCSANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGYKLYQYMH 240
 QY 241 PLCGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLPESFICKELGENVANIYKD 300
 Db 241 PLCGSSATLTCVPLGNLIVN ----- 262
 QY 301 LQKLSRLFKQOLYPLIAFTRQALNLPDVFGVLVPLLEKLRIFFRLDVRSVLSAVCR 360
 Db 263 -----ALNLPDVFGVLVPLLEKLRIFFRLDVRSVLSAVCR 300
 QY 361 DLFTASNDPLLMRFYLDRDPRDNTVRVQDTWKELVYKRIQRKSPKGRFVWMLPSSTH 420
 Db 301 DLFTASNDPLLMRFYLDRDPRDNTVRVQDTWKELVYKRIQRKSPKGRFVWMLPSSTH 360
 QY 421 TTFYPNPLHRRPPSSRLPPGIIGGEYDQPTLPYVGDPISSLPDGPETPSQFPPLRP 480
 Db 361 TTFYPNPLHRRPPSSRLPPGIIGGEYDQPTLPYVGDPISSLPDGPETPSQFPPLRP 420
 QY 481 RFDVPGPLPGPNPLIPGRGPNDRFPFRPSRGRPTDGRLSFM 522
 Db 421 RFDVPGPLPGPNPLIPGRGPNDRFPFRPSRGRPTDGRLSFM 462

RESULT 8

US-09-397-945-435
 ; Sequence 435, Application US/09397945
 ; Publication No. US2003005139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc. et al.
 ; TITLE OF INVENTION: 95 Human secreted proteins
 ; FILE REFERENCE: P2027P1
 ; CURRENT APPLICATION NUMBER: US/09/397, 945
 ; PRIOR APPLICATION NUMBER: PCT/US99/05804
 ; PRIOR FILING DATE: 1999-03-18
 ; PRIOR APPLICATION NUMBER: 60/078, 566
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/078, 576
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/078, 573
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/078, 574
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/078, 579
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/080, 314
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080, 312
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/078, 578
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/078, 581
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/078, 577
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/078, 563
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/080, 313
 ; PRIOR FILING DATE: 1998-04-01
 ; NUMBER OF SEQ ID NOS: 470
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 435
 ; LENGTH: 497
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (150)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-397-945-435

Query Match 87.3%; Score 2404; DB 10; Length 497;
 Best Local Similarity 88.1%; Pred. No. 1,4e-193;
 Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
 QY 1 MELRVRLKRTMPLEVPETPTGLRSHRLSLICTGVSSNRPFTITLYKDDLTGDE 60
 Db 36 MELRVRLKRTMPLEVPETPTGLRSHRLSLICTGVSSNRPFTITLYKDDLTGDE 95
 QY 61 ETLASGVISGDLICLLIIDDIPAPNIPSSDSEHSSLQNNQPSLATSNOTSQDQOP 120
 Db 96 ETLASGVISGDLICLLIIDDIPAPNIPSSDSEHSSLQNNQPSLATSNOTSQDQOP 155
 QY 121 SDFQQAAGGVWVNDSDMLGPSQNFENSIQDNAMAEGETGYPSPHMLCSSEVGGVP 180
 Db 156 SDFQQAAGGVWVNDSDMLGPSQNFENSIQDNAMAEGETGYPSPHMLCSSEVGGVP 215
 QY 181 HSELTLYQSADCSANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGYKLYQYMH 240
 Db 216 HSELTLYQSADCSANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGYKLYQYMH 275
 QY 241 PLCGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLPESFICKELGENVANIYKD 300
 Db 276 PLCGSSATLTCVPLGNLIVN ----- 297
 QY 301 LQKLSRLFKQOLYPLIAFTRQALNLPDVFGVLVPLLEKLRIFFRLDVRSVLSAVCR 360
 Db 298 -----ALNLPDVFGVLVPLLEKLRIFFRLDVRSVLSAVCR 335
 QY 361 DLFTASNDPLLMRFYLDRDPRDNTVRVQDTWKELVYKRIQRKSPKGRFVWMLPSSTH 420
 Db 336 DLFTASNDPLLMRFYLDRDPRDNTVRVQDTWKELVYKRIQRKSPKGRFVWMLPSSTH 395
 QY 421 TTFYPNPLHRRPPSSRLPPGIIGGEYDQPTLPYVGDPISSLPDGPETPSQFPPLRP 480
 Db 396 TTFYPNPLHRRPPSSRLPPGIIGGEYDQPTLPYVGDPISSLPDGPETPSQFPPLRP 455
 QY 481 RFDVPGPLPGPNPLIPGRGPNDRFPFRPSRGRPTDGRLSFM 522
 Db 456 RFDVPGPLPGPNPLIPGRGPNDRFPFRPSRGRPTDGRLSFM 497

RESULT 9

US-10-653-595-435
 ; Sequence 435, Application US/10653595
 ; Publication No. US20040046304A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et. al.
 ; TITLE OF INVENTION: 95 Human secreted proteins
 ; FILE REFERENCE: P2027P1C1
 ; CURRENT APPLICATION NUMBER: US/10/653, 595
 ; PRIOR APPLICATION NUMBER: US 09/397945
 ; PRIOR FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: PCT/US99/05804
 ; PRIOR FILING DATE: 1999-03-18
 ; PRIOR APPLICATION NUMBER: 60/078, 566
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/078, 576
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/078, 573
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/078, 574
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/078, 579
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 60/080, 314
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080, 312
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/078, 578
 ; PRIOR FILING DATE: 1998-03-19

Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 435
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (150)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-653-595-435

Query Match 87.3%; Score 2404; DB 15; Length 497;
Best Local Similarity 88.1%; Pred. No. 1,4e-193;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLVRLKRTWPEVETETPTLGHLSHRLSLICLQWGSSTNRPFTLTNYDPLTQDE 60
DB 36 MRLVRLKRTWPEVETETPTLGHLSHRLSLICLQWGSSTNRPFTLTNYDPLTQDE 95
QY 61 ETLASVIGSDLLICLLDIPAPNIPSSSTDSHSSLQNNQPSLATSSNQTSGODEQ 120
DB 96 ETLASVIGSDLLICLLDIPAPNIPSSSTDSHSSLQNNQPSLATSSNQTSGODEQ 155
QY 121 SDSFGQAAGSGVNDSDMLGPSQNFASISQDNAMAEAGTGFYSEPMLCSSVEGQVP 180
DB 156 SDSFGQAAGSGVNDSDMLGPSQNFASISQDNAMAEAGTGFYSEPMLCSSVEGQVP 215
QY 181 HSELTIVQADCSNDALIVLHILMLESGYIPQCTEAKALSMPEKMLSGYKQYMH 240
DB 216 HSELTIVQADCSNDALIVLHILMLESGYIPQCTEAKALSMPEKMLSGYKQYMH 275
QY 241 PLGSSSATLTQVPLGNLIYVNAATLKINNEIRSVKRLQLPESFICKELGENVANITYK 300
DB 276 PLGSSSATLTQVPLGNLIYVNAATLKINNEIRSVKRLQLPESFICKELGENVANITYK 297
QY 301 LQKLSRLFKDQVYPLAFLRQALNLPDVGELYVLPLELKLRIPLLDVSVLSAVCR 360
DB 298 -----ALNPDVGELYVLPLELKLRIPLLDVSVLSAVCR 335
QY 361 DLFTASNDPLLMRLYLRFEDNTTVRVQDTWKELYKRKHIOKRESKGFVMLPES 420
DB 336 DLFTASNDPLLMRLYLRFEDNTTVRVQDTWKELYKRKHIOKRESKGFVMLPES 395
QY 421 TTPYVNPILHRRPSSSLPPGILIGGYDORPTLVYGDPISSILPPGPTPSQFPPLRP 480
DB 396 TTPYVNPILHRRPSSSLPPGILIGGYDORPTLVYGDPISSILPPGPTPSQFPPLRP 455
QY 481 RFDVPGPLGPNPILPGRGPNDRFPFRPSKGRPTDRLSPM 522
DB 456 RFDVPGPLGPNPILPGRGPNDRFPFRPSKGRPTDRLSPM 497

RESULT 10
US-10-679-246-8
; Sequence 8, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679, 246
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 443
; TYPE: PRT

; ORGANISM: Homo sapien
US-10-679-246-8
Query Match 82.4%; Score 2270; DB 16; Length 443;
Best Local Similarity 99.8%; Pred. No. 2,4e-182;
Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 92 DSEHSSLQNNQPSLATSSNQTSGODEQPSDFGQAAGSGVNDSDMLGPSQNFASIS 151
DB 13 DSEHSSLQNNQPSLATSSNQTSGODEQPSDFGQAAGSGVNDSDMLGPSQNFASIS 72
QY 152 QDNAMAEAGTGFYSEPMLCSSVEGQVPHLETLVQADCSNDALIVLHILMLESG 211
DB 73 QDNAMAEAGTGFYSEPMLCSSVEGQVPHLETLVQADCSNDALIVLHILMLESG 132
QY 212 YIPQCTEAKALSMPEKMLSGYKQYMHPLCESSSATLTQVPLGNLIYVNAATLKINNEI 271
DB 133 YIPQCTEAKALSMPEKMLSGYKQYMHPLCESSSATLTQVPLGNLIYVNAATLKINNEI 192
QY 272 RSVKRLQLPESFICKELGENVANITYKDLKLSRLFDQOLVYPLAFLRQALNLPDVG 331
DB 193 RSVKRLQLPESFICKELGENVANITYKDLKLSRLFDQOLVYPLAFLRQALNLPDVG 252
QY 332 LVVLPLELKLRIPLLDVRSVLSAVCRDLFTASNDPLLMRLYLRFEDNTTVRVQDT 391
DB 253 LVVLPLELKLRIPLLDVRSVLSAVCRDLFTASNDPLLMRLYLRFEDNTTVRVQDT 312
QY 392 WKELYKRKHIOKRESKGRFVMLPSSSTHTTPTFPNPLHRRPSSSLPPGILIGGYDOR 451
DB 313 WKELYKRKHIOKRESKGRFVMLPSSSTHTTPTFPNPLHRRPSSSLPPGILIGGYDOR 372
QY 452 PTLFYVGPPISSILPGRGPTPSQFPPLRPDRDPVGPLGPNILPGRGPNDRFPFRPSR 511
DB 373 PTLFYVGPPISSILPGRGPTPSQFPPLRPDRDPVGPLGPNILPGRGPNDRFPFRPSR 432
QY 512 GRPTDRLSPM 522
DB 433 GRPTDRLSPM 443

RESULT 11
US-10-264-237-2484
; Sequence 2484, Application US/10264237
; Publication No. US2004009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2484
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2484

Query Match 55.4%; Score 1527; DB 15; Length 317;
Best Local Similarity 94.0%; Pred. No. 6,1e-120;
Matches 300; Conservative 4; Mismatches 11; Indels 4; Gaps 2;

QY 115 MDEQPSDFGQAAGSGVNDSDMLGPSQNFASISQDNAMAEAGTGFYSEPMLCSS 174
DB 1 MDEQPSDFGQAAGSGVNDSDMLGPSQNFASISQDNAMAEAGTGFYSEPMLCSS 60
QY 175 VEGQVPHSLETLVQADCSNDALIVLHILMLESGYIPQCTEAKALSMPEKMLSGY 234
DB 61 VEGQVPHSLETLVQADCSNDALIVLHILMLESGYIPQCTEAKALSMPEKMLSGY 120

Tue Nov 16 07:54:47 2004

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Page 7

Qy	233	KIQYMHPLCGSSAATITCTVPLGNLIVVNAATLKINNEISVYRLDLPBSFICKEKLGENV	294
Db	121	KIQYMHPLCGSSAATITCTVPLGNLIVVNAATLKINNEISVYRLDLPBSFICKEKLGENV	180
Qy	295	ANIYKDLQKLSRFLFQDLYVPLLAFTROALNPDEVFGVLVPLELKIIRIFLLDVRVLS	354
Db	181	ANIYKDLQKLSRFLFQDLYVPLLAFTROALNPDEVFGVLVPLELKIIRIFLLDVRVLS	240
Qy	355	LSAVCSDLFTASNDPLIMRFLYLRDFRNDTVAVQDTWKELYRKRIQRKESPKGRF-V	412
Db	241	LSAVCSDDLFTASNDPLIMRFLYLRDFRNDTVAVQDTWKELYRKRIQRKESPKGRVCA	300
Qy	413	MLPSSHTLIPFYNPLHP	431
Db	301	PAIVNSHSTL-ISQPLAP	317

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RESULT 12
US-10-408-765A-752
; Sequence 752, Application US/10/408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 752
; LENGTH: 231
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-408-765A-752

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	Query Match	45.0%	Score 1238	DB 16	Length 231
	Best Local Similarity	100.0%	Pred. No. 8.7e-36		
	Matches 231	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	292	ENVANIYKDLOKLSRLFDQIVYPLLAFTROALNPVDFGIWVLEPLKLRIFRLDVS	351		
Db	1	ENVANIYKDLOKLSRLFDQIVYPLLAFTROALNPVDFGIWVLEPLKLRIFRLDVS	60		
QY	352	VLSLSAVCDLFLASNDPLLMRFLLTRPFQNTYRVODTWKELYRGRHQRKESKGF	411		
Db	61	VLSLSAVCDLFLASNDPLLMRFLLTRPFQNTYRVODTWKELYRGRHQRKESKGF	120		
QY	412	VMLLPSTHTIFYPNPLHRRPFSSRLPCGIGEVQDRPLPYVCDPISLIPPGRT	471		
Db	121	VMLLPSTHTIPYPNPLHRRPFSSRLPCGIGEVQDRPLPYVCDPISLIPPGRT	180		
QY	472	PSGFPPLRRPDPVGPLPGEPNILTRGGQPNDRPPFRSSRGRPDGSLSPV	522		
Db	181	PSGFPPLRRPDPVGPLPGEPNILTRGGQPNDRPPFRSSRGRPDGSLSPV	231		

RESULT 13
US-10-094-749-1723
; Sequence 1723, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI

```

? APPLICANT: SATO, HIROYUKI
? APPLICANT: ISHII, SHIZUKO
? APPLICANT: YAMAMOTO, JUN-ICHI
? APPLICANT: ISONO, YUUKO
? APPLICANT: HIO, YURI
? APPLICANT: OTSUKA, KAORU
? APPLICANT: NAGAI, KEIICHI
? APPLICANT: IRIE, RYOTARO
? APPLICANT: TAMECHIKA, ICHIRO
? APPLICANT: SEKI, NAOHICO
? APPLICANT: YOSHIKAWA, TSUTOMU
? APPLICANT: OTSUKA, MOTOKUKI
? APPLICANT: NAGAHARI, KENJI
? APPLICANT: MASUHO, YASUHIKO
? TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
? FILE REFERENCE: 084335/0160
? CURRENT APPLICATION NUMBER: US/10/094,749
? CURRENT FILING DATE: 2002-03-12
? PRIOR APPLICATION NUMBER: 60/350,435
? PRIOR FILING DATE: 2002-01-24
? PRIOR APPLICATION NUMBER: JP 2001-328381
? PRIOR FILING DATE: 2001-09-14
? NUMBER OF SEQ ID NOS: 3381
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 1723
? LENGTH: 221
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-10-094-749-1723

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	Query Match	39.4%	Score 1086	DB 14	Length 221	Best Local Similarity	93.1%	Pred. No. 5	283	Matches 203	Conservative	4	Mismatches	7	Indels	4	Gaps	1
Qy	KDCQVYPLIATR---	CA	LT	LP	VG	IV	PL	EK	UR	IP	LD	VS	YLS	SA	VR	DL	PT	364
Db	KPDVLYEVIPTSL	FL	LA	NT	LP	VG	IV	PL	EK	UR	IP	LD	VS	YLS	SA	VR	DL	63
Qy	309	KDCQVYPLIATR---	CA	LT	LP	VG	IV	PL	EK	UR	IP	LD	VS	YLS	SA	VR	DL	364
Db	4	KPDVLYEVIPTSL	FL	LA	NT	LP	VG	IV	PL	EK	UR	IP	LD	VS	YLS	SA	VR	63
Qy	365	ASNPDLMRP	LY	LD	FR	NT	YR	VD	T	M	K	E	L	Y	R	K	H	424
Db	64	ASNPDLMRP	LY	LD	FR	NT	YR	VD	T	M	K	E	L	Y	R	K	H	123
Qy	425	YPNLHRRP	P	P	S	S	L	P	Q	I	G	E	Y	D	R	T	L	484
Db	124	YPNLHRRP	P	P	S	S	L	P	Q	I	G	E	Y	D	R	T	L	183
Qy	485	VGPLPGRNP	L	P	GR	G	P	ND	R	P	P	R	P	S	R	G	P	522
Db	184	VGPLPGRNP	L	P	GR	G	P	ND	R	P	P	R	P	S	R	G	P	221

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1 RESULT 14
2 US-09-197-945-434
3 Sequence 434, Application US/05397945
4 Publication No. US20030065139A1
5 GENERAL INFORMATION:
6 APPLICANT: Human Genome Sciences, Inc. et al.
7 TITLE OF INVENTION: 95 Human secreted proteins
8 FILE REFERENCE: P2027P1
9 CURRENT APPLICATION NUMBER: US/09/197,945
10 CURRENT FILING DATE: 1999-09-17
11 PRIOR APPLICATION NUMBER: PCT/US99/05804
12 PRIOR FILING DATE: 1999-03-18
13 PRIOR APPLICATION NUMBER: 60/078,566
14 PRIOR FILING DATE: 1998-03-19
15 PRIOR APPLICATION NUMBER: 60/078,576
16 PRIOR FILING DATE: 1998-03-19
17 PRIOR APPLICATION NUMBER: 60/078,573
18 PRIOR FILING DATE: 1998-03-19
19 PRIOR APPLICATION NUMBER: 60/078,574
20 PRIOR FILING DATE: 1998-03-19
21 PRIOR APPLICATION NUMBER: 60/078,579
22 PRIOR FILING DATE: 1998-03-19

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; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 434
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-945-434

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Query Match      25.9%; Score 714; DB 10; Length 174;
Best Local Similarity 100.0%; Pred. No. 8.3e-52;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 395 LYRKHIOKESPKGRFVMLLPSSHTTIPFYNPPLHPRPPSSRLPGIIGGEYDQRTL 454
    |||||||
Db 47 LYRKHIOKESPKGRFVMLLPSSHTTIPFYNPPLHPRPPSSRLPGIIGGEYDQRTL 106
    |||||||
QY 455 PYVGDPISSLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSRGRP 514
    |||||||
Db 107 PYVGDPISSLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSRGRP 166
    |||||||
QY 515 TDGRLSFM 522
    |||||||
Db 167 TDGRLSFM 174
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RESULT 15
US-10-653-595-209
; Sequence 209, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1C1
; CURRENT APPLICATION NUMBER: US/10/653,595
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 209

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; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-653-595-209

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Query Match      25.9%; Score 714; DB 15; Length 174;
Best Local Similarity 100.0%; Pred. No. 8.3e-52;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 395 LYRKHIOKESPKGRFVMLLPSSHTTIPFYNPPLHPRPPSSRLPGIIGGEYDQRTL 454
    |||||||
Db 47 LYRKHIOKESPKGRFVMLLPSSHTTIPFYNPPLHPRPPSSRLPGIIGGEYDQRTL 106
    |||||||
QY 455 PYVGDPISSLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSRGRP 514
    |||||||
Db 107 PYVGDPISSLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSRGRP 166
    |||||||
QY 515 TDGRLSFM 522
    |||||||
Db 167 TDGRLSFM 174
    |||||||

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Search completed: November 16, 2004, 07:24:24
Job time : 143 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 06:56:14 ; Search time 39 Seconds
(without alignments)
887,641 Million cell updates/sec

Title: US-09-927-458-2

2754

Perfect score: 1 MLRLVRLKRTWPLEVETET.....DRFPFRSGRGTDLGSLFM 522

Sequence:

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A COMB .pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB .pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB .pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB .pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB .pep.*
6: /cgn2_6/ptodata/1/iaa/backfitted .pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2744	99.6	522	4	US-09-591-694-10 Sequence 10, Appl
2	2489	90.4	482	4	US-09-385-219A-14 Sequence 16, Appl
3	2270	82.4	443	4	US-09-591-694-6 Sequence 8, Appl1
4	553	20.1	102	4	US-09-621-976-5935 Sequence 5355, Ap
5	194	7.0	39	4	US-09-385-219A-21 Sequence 21, Appl
6	189	6.9	38	3	US-09-172-841-47 Sequence 47, Appl
7	189	6.9	38	4	US-08-951-621-47 Sequence 47, Appl
8	164	6.0	38	3	US-09-172-841-49 Sequence 49, Appl
9	164	6.0	38	4	US-08-951-621-49 Sequence 49, Appl
10	144	5.0	321	4	US-09-166-350-15 Sequence 15, Appl
11	139	5.0	327	4	US-09-591-694-12 Sequence 12, Appl
12	139	5.0	327	4	US-09-385-219A-58 Sequence 58, Appl
13	117.5	4.3	503	4	US-09-599-287A-2 Sequence 2, Appl1
14	117	4.2	507	4	US-09-599-287A-24 Sequence 24, Appl
15	112	4.1	690	4	US-09-248-796A-19169 Sequence 19169, A
16	110	4.0	424	4	US-09-538-092-1338 Sequence 1338, Ap
17	107.5	3.9	776	4	US-09-252-981A-28446 Sequence 28446, A
18	107	3.9	78	1	US-08-487-359-5 Sequence 5, Appl1
19	107	3.9	78	1	US-08-222-798A-5 Sequence 5, Appl1
20	107	3.9	489	4	US-09-543-681A-7388 Sequence 7388, Ap
21	105	3.8	297	4	US-09-252-991A-29217 Sequence 29217, A
22	104	3.8	1312	4	US-09-554-572-26 Sequence 26, Appl
23	103.5	3.8	79	1	US-08-487-359-8 Sequence 8, Appl1
24	103.5	3.8	79	1	US-08-222-798A-8 Sequence 8, Appl1
25	103.5	3.8	580	3	US-08-906-865-1 Sequence 1, Appl1
26	103.5	3.8	580	4	US-09-129-668-1 Sequence 1, Appl1
27	103.5	3.8	888	2	US-08-861-464-6 Sequence 6, Appl1

28	103.5	3.8	888	2	US-08-396-001-6 Sequence 6, Appl1
29	103.5	3.8	888	3	US-09-323-433A-6 Sequence 6, Appl1
30	103.5	3.8	888	4	US-09-826-752-6 Sequence 6, Appl1
31	103	3.7	133	4	US-09-252-991A-21490 Sequence 21490, A
32	103	3.7	431	4	US-09-248-796A-17260 Sequence 17260, A
33	102.5	3.7	79	1	US-08-487-359-2 Sequence 2, Appl1
34	102.5	3.7	79	1	US-08-222-798A-2 Sequence 2, Appl1
35	102.5	3.7	644	4	US-09-198-452A-822 Sequence 822, App
36	102	3.7	141	4	US-09-270-767-38716 Sequence 38716, A
37	102	3.7	141	4	US-09-270-767-53933 Sequence 53933, A
38	102	3.7	626	4	US-09-345-473E-43 Sequence 43, Appl
39	102	3.7	683	3	US-09-213-293D-1 Sequence 1, Appl1
40	102	3.7	866	4	US-09-527-084A-4 Sequence 4, Appl1
41	101.5	3.7	261	4	US-09-270-767-46755 Sequence 46755, A
42	101.5	3.7	1149	3	US-08-560-005-5 Sequence 5, Appl1
43	101.5	3.7	1149	4	US-09-418-540-5 Sequence 5, Appl1
44	101.5	3.7	1149	4	US-09-969-528-5 Sequence 5, Appl1
45	101	3.7	501	4	US-09-270-767-43743 Sequence 43743, A

ALIGNMENTS

RESULT 1
US-09-591-694-10
; Sequence 10, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: Udm C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: In Protein Degradation, Products and Methods Related Thereo
; FILE REFERENCE: P-12 4220
; CURRENT APPLICATION NUMBER: US/09/591, 694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330, 517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-10

Query Match 99.6%; Score 2744; DB 4; Length 522;
Best Local Similarity 99.6%; Pred. No. 36-255;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLRLVRLKRTWPLEVETETPTLGHLSRLVSLICVWGSNTPTTLNKDPLTGD 60
1 MLRLVRLKRTWPLEVETETPTLGHLSRLVSLICVWGSNTPTTLNKDPLTGD 60
Db 61 HTLASGVISGLICILLODDIPAPNIPSTSTSEHSLONNOPSLATSNQTSMDROP 120
61 HTLASGVISGLICILLODDIPAPNIPSTSTSEHSLONNOPSLATSNQTSMDROP 120
QY 121 SPSFGQAAGSVMNDMSMLGPSQNFSAESIODNAHMAEGTFYSEPMKCSSEVGGQVP 180
121 SPSFGQAAGSVMNDMSMLGPSQNFSAESIODNAHMAEGTFYSEPMKCSSEVGGQVP 180
Db 121 SPSFGQAAGSVMNDMSMLGPSQNFSAESIODNAHMAEGTFYSEPMKCSSEVGGQVP 180
121 SPSFGQAAGSVMNDMSMLGPSQNFSAESIODNAHMAEGTFYSEPMKCSSEVGGQVP 180
QY 181 HSEFTLYGASDSDANDALIVLHLMESGYIPGTEKALSMPEKMLSGVYLQVYH 240
181 HSEFTLYGASDSDANDALIVLHLMESGYIPGTEKALSMPEKMLSGVYLQVYH 240
Db 181 HSEFTLYGASDSDANDALIVLHLMESGYIPGTEKALSMPEKMLSGVYLQVYH 240
181 HSEFTLYGASDSDANDALIVLHLMESGYIPGTEKALSMPEKMLSGVYLQVYH 240
QY 241 PCEGSSATLTCVPLGNLIVNATLKINNEISVRLQLLPESFICKEKLGENVANIYKD 300
241 PCEGSSATLTCVPLGNLIVNATLKINNEISVRLQLLPESFICKEKLGENVANIYKD 300
Db 241 PCEGSSATLTCVPLGNLIVNATLKINNEISVRLQLLPESFICKEKLGENVANIYKD 300
241 PCEGSSATLTCVPLGNLIVNATLKINNEISVRLQLLPESFICKEKLGENVANIYKD 300
QY 301 LQKLSLTFDQVYPLATFRQALNLPDVFGLVPLPEKLRIFFLDVRVSLISAVCR 360
301 LQKLSLTFDQVYPLATFRQALNLPDVFGLVPLPEKLRIFFLDVRVSLISAVCR 360
Db 301 LQKLSLTFDQVYPLATFRQALNLPDVFGLVPLPEKLRIFFLDVRVSLISAVCR 360
301 LQKLSLTFDQVYPLATFRQALNLPDVFGLVPLPEKLRIFFLDVRVSLISAVCR 360

QY 361 DLFTASNDPLLMRLFLYLDFDNDTVAVDTWKEIYKRRHIQRKESPKGRFVMLPESSTH 420
DB 361 DLFTASNDPLLMRLFLYLDFDNDTVAVDTWKEIYKRRHIQRKESPKGRFVMLPESSTH 420
QY 421 TTFPVNPLHPRPFPSSRLPGIIGGEYDORPTLPYVGPDISSILPGSGEPSPQFPPLRP 480
DB 421 TTFPVNPLHPRPFPSSRLPGIIGGEYDORPTLPYVGPDISSILPGSGEPSPQFPPLRP 480
QY 481 RFDVGPPLGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
DB 481 RFDVGPPLGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522

RESULT 2

US-09-385-219A-14
; Sequence 14, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiatour, D.
; APPLICANT: Pagano, M.
; APPLICANT: Laties, S.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-14

Query Match 90.4%; Score 2489; DB 4; Length 482;
Best Local Similarity 98.1%; Pred. No. 9.5e-231;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 42 SNTRETTITLANKDPLTGTDEETLASGYISGDLICLILODDIPAPNIPESSTDESHSLQNN 101
DB 2 SNTRETTITLANKDPLTGTDEETLASGYISGDLICLILODDIPAPNIPESSTDESHSLQNN 61
QY 102 EOPSLATSSNOTSMODEQPSDSFOGQAQSGVWMDSDMLGSPQNFEEASIQDNHMAEGT 161
DB 62 EOPSLATSSNOTSIQDEQPSDSFOGQAQSGVWMDSDMLGSPQNFEEASIQDNHMAEGT 121
QY 162 GFYSPAPMLCSSEVGGQVPHSLLETLYQSGADCSANDALIVLHILMLESGYIPQGTBAKA 221
DB 122 GFYSPAPMLCSSEVGGQVPHSLLETLYQSGADCSANDALIVLHILMLESGYIPQGTBAKA 181
QY 222 LSMPEKWKLSGVYKLYQWHPICEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP 281
DB 182 LSMPEKWKLSGVYKLYQWHPICEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP 241
QY 282 ESFICEKXKGENVANIYKDLQKLSRLFKDQLVYPLLAFTROALNLPVFGVLVPLEKXL 341
DB 242 ESFICEKXKGENVANIYKDLQKLSRLFKDQLVYPLLAFTROALNLPVFGVLVPLEKXL 301
QY 342 RIFRLLDVRSVLSISAVCRDLFTASNDPLLMRLFLYLDFDNDTVAVDTWKEIYKRRHI 401
DB 302 RIFRLLDVRSVLSISAVCRDLFTASNDPLLMRLFLYLDFDNDTVAVDTWKEIYKRRHI 361
QY 402 QRKESPKGRFVMLPESSTHTTIPYVNPPLHPRPFPSSRLPGIIGGEYDORPTLPYVGPDI 461
DB 362 QRKESPKGRFVMLPESSTHTTIPYVNPPLHPRPFPSSRLPGIIGGEYDORPTLPYVGPDI 421
QY 462 SSLIPGEPETPSQFPPLRPREDPVGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 521
DB 521 SSLIPGEPETPSQFPPLRPREDPVGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 481

DB 422 SSLIPGEPETPSQFPPLRPREDPVGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 481
QY 522 M 522
DB 482 M 482

RESULT 3

US-09-591-694-8
; Sequence 8, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: In Protein Degradation, Products and Methods Related Thereof
; FILE REFERENCE: P-Lt 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; PRIOR FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-8

Query Match 82.4%; Score 2270; DB 4; Length 443;
Best Local Similarity 99.8%; Pred. No. 1e-209;
Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 92 DSEHSLQNNRQPSLATSSNOTSMODEQPSDSFOGQAQSGVWMDSDMLGSPQNFEEASI 151
DB 13 DSEHSLQNNRQPSLATSSNOTSMODEQPSDSFOGQAQSGVWMDSDMLGSPQNFEEASI 72
QY 152 QDNHMAEGTGFYSPAPMLCSSEVGGQVPHSLLETLYQSGADCSANDALIVLHILMLESG 211
DB 73 QDNHMAEGTGFYSPAPMLCSSEVGGQVPHSLLETLYQSGADCSANDALIVLHILMLESG 132
QY 212 YIPQGTBAKALSMPEKWKLSGVYKLYQWHPICEGSSATLTCVPLGNLIVNATLKINNEI 271
DB 133 YIPQGTBAKALSMPEKWKLSGVYKLYQWHPICEGSSATLTCVPLGNLIVNATLKINNEI 192
QY 272 RSVKRLQLLPESFICEKXKGENVANIYKDLQKLSRLFKDQLVYPLLAFTROALNLPVFG 331
DB 193 RSVKRLQLLPESFICEKXKGENVANIYKDLQKLSRLFKDQLVYPLLAFTROALNLPVFG 252
QY 332 LVYVPLEKXLRIFRLLDVRSVLSISAVCRDLFTASNDPLLMRLFLYLDFDNDTVAVDT 391
DB 253 LVYVPLEKXLRIFRLLDVRSVLSISAVCRDLFTASNDPLLMRLFLYLDFDNDTVAVDT 312
QY 392 WKELIYKRRHIQRKESPKGRFVMLPESSTHTTIPYVNPPLHPRPFPSSRLPGIIGGEYDOR 451
DB 313 WKELIYKRRHIQRKESPKGRFVMLPESSTHTTIPYVNPPLHPRPFPSSRLPGIIGGEYDOR 372
QY 452 PTLVYVGDPISSILPGSGEPSPQFPPLRPREDPVGPLPGPNPILPGRGPNDRPFRPSR 511
DB 373 PTLVYVGDPISSILPGSGEPSPQFPPLRPREDPVGPLPGPNPILPGRGPNDRPFRPSR 432
QY 512 GRPTDGRLSFM 522
DB 433 GRPTDGRLSFM 443

RESULT 4

US-09-621-976-5935
; Sequence 5935, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.

APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET, 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5935
LENGTH: 102
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 87
OTHER INFORMATION: Xaa = Cys, Gly
US-09-621-976-5935

Query Match 20.1%; Score 553; DB 4; Length 102;
Best Local Similarity 99.0%; Pred. No. 1,9e-45;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 413 MLPSSTHTTTPFYNPPLHPRFPSSRLPPGIGGYDQPTLPYVGDPISSLLPGQETP 472

DB 1 MLPSSTHTTTPFYNPPLHPRFPSSRLPPGIGGYDQPTLPYVGDPISSLLPGQETP 60

QY 473 SQFPPLRPRFPDVPGLPGPNPILPGRGQPNDRPFPRSR 511

DB 61 SQFPPLRPRFPDVPGLPGPNPILPGRGQPNDRPFPRSR 99

RESULT 5
US-09-385-219A-21
Sequence 21, Application US/09385219A
Patent No. 6720181
GENERAL INFORMATION:
APPLICANT: Chaur, D.
APPLICANT: Pagano, M.
APPLICANT: Latres, E.
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
FILE REFERENCE: 5914-081
CURRENT APPLICATION NUMBER: US/09/385,219A
CURRENT FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/098,355
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 60/118,568
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: 60/124,449
PRIOR FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
US-09-385-219A-21

Query Match 7.0%; Score 194; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLDVRSVLSAVCRDLFTASNDPLWR 373

DB 1 LPLEKLRIFRLDVRSVLSAVCRDLFTASNDPLWR 39

RESULT 6
US-09-172-841-47
Sequence 47, Application US/09172841
Patent No. 623081
GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Elledge, Stephen J.
TITLE OF INVENTION: F-BOX PROTEINS AND GENES

FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/172,841
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 47
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-172-841-47

Query Match 6.9%; Score 189; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLDVRSVLSAVCRDLFTASNDPLWR 372

DB 1 LPLEKLRIFRLDVRSVLSAVCRDLFTASNDPLWR 38

RESULT 7
US-08-951-621-47
Sequence 47, Application US/08951621
Patent No. 6573094
GENERAL INFORMATION:
APPLICANT: HARPER, JEFFREY W.
APPLICANT: ELLEDGE, STEPHEN J.
TITLE OF INVENTION: F-BOX GENES AND PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,621
FILING DATE: 16-OCT-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: BCM-02999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-951-621-47

Query Match 6.9%; Score 189; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLDVRSVLSAVCRDLFTASNDPLWR 372

DB 1 LPLEKLRIFRLDVRSVLSAVCRDLFTASNDPLWR 38

RESULT 8

US-09-172-841-49
; Sequence 49, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; APPLICANT: Elledge, Stephen J.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 49
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-172-841-49
Query Match 6.0%; Score 164; DB 3; Length 38;
Best Local Similarity 86.8%; Pred. No. 1,1e-08;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 335 LPLEKLRIFRLDVRSLISAVCRDLFTASNDPLIM 372
DB 1 LPLEKLRIFRLDVRSLISAVCRDLFTASNDPLIM 38
RESULT 9
US-08-951-621-49
; Sequence 49, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; APPLICANT: ELLEDGE, STEPHEN J.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,621
; FILING DATE: 16-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Karlin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: BCM-02999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-951-621-49
Query Match 6.0%; Score 164; DB 4; Length 38;
Best Local Similarity 86.8%; Pred. No. 1,1e-08;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLDVRSLISAVCRDLFTASNDPLIM 372
DB 1 LPLEKLRIFRLDVRSLISAVCRDLFTASNDPLIM 38
RESULT 10
US-09-166-350-15
; Sequence 15, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 15
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-350-15
Query Match 5.2%; Score 144; DB 4; Length 321;
Best Local Similarity 23.1%; Pred. No. 3e-05;
Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;
QY 233 VKKQYMPHLECG--SSALTTCVPL---GNLVNATLKINNE-----IRSV-- 274
DB 35 MFRQMMFELAGVSSNLENKPCPRARGSLQKTSADTKGQEOAKERAEFLKAVEE 94
QY 275 -----KRLDLP-----SFICKKIGENVANYI---KDLQKLSRL---FK 309
DB 95 EONGALYEAIKFRRAMQVPEIEKITYTSSPDGDGNGNIENDDSGMADLSYFQ 154
QY 310 DQLYVPLLAFTROALNL--PDV---FGLVPLLEKLRIRRL-----LDVRSVLSAV 358
DB 155 QQ-----LTFQESVYKLCPHELSSQIHISVLPMEVLYIFRWVSSDLDRSLQSLV 209
QY 359 CRDLFTASNDPLIMRFYLRDRDNTVR--VQTDKKEIYRKRIKESPKGRFYMLPS 417
DB 210 CGFYICARDPEIWLACKVWGRCIKVPTYSKREMPLE-----PVRFPGYIIS 262
QY 418 ST-----HTIPFYPNPMPHPFPSSRLPGIIGGEYDQRPFLPYVGD 460
DB 263 KTTYIRQSGQSLDGFYRAMHQVEY--RYIRFPFDGHV----- 298
QY 461 ISSLIPGPGETSGPPPLRPR 481
DB 299 --MULTPEEPOSTIVRLRTR 317
RESULT 11
US-09-591-694-12
; Sequence 12, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; CURRENT FILING DATE: 2000-06-09

EARLIER APPLICATION NUMBER: US 09/330,517
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapien
US-09-591-694-12

Query Match 5.0%; Score 139; DB 4; Length 327;
Best Local Similarity 25.1%; Pred. No. 9.5e-05;
Matches 57; Conservative 32; Mismatches 64; Indels 74; Gaps 11;

QY 291 GENVANYI---KDLQKLSRL---FKDQVYPLLAFTROALNT---PDV---FGLVVLPL 337
DB 19 GDGVGNSYIEDNDSDSKADLISYFCQ---LTFQESVTKLQCPBELSSQIHISVLPM 73
QY 338 ELKLRIRL---LDVRSVLSAVCRDLFTASNDPLMRFLYLRDPDNTVR-VQDD 391
DB 74 EVMWYIFRWVSSDLDRSLSEQLSVCRGFYICARDEIWRACLKMGSSCIKLVYYS 133
QY 392 WKELYRKRIQRKSPKGRFVMLLPSSST---HTIPYPNPLPRPF 434
DB 134 WREWFLEL---PVRFDGVYISKTYIROEGSLDGFYRAMQVEY---RYIRFF 183
QY 435 PSSRLPGIIGGYDQRPFLPYVGDPLSLIPGSGETPSQFPLRPF 481
DB 184 PDGHV-----MMLTPEEPQSIYPRLRTR 207

RESULT 12
US-09-385-219A-58
Sequence 58; Application US/09385219A
Patent No. 6720181
GENERAL INFORMATION:
APPLICANT: Chateau, D.
APPLICANT: Pasano, M.
APPLICANT: Latres, E.
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
FILE REFERENCE: 5814-081
CURRENT APPLICATION NUMBER: US/09/385,219A
CURRENT FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/098,355
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 60/118,568
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: 60/124,449
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-385-219A-58

Query Match 5.0%; Score 139; DB 4; Length 327;
Best Local Similarity 25.1%; Pred. No. 9.5e-05;
Matches 57; Conservative 32; Mismatches 64; Indels 74; Gaps 11;
QY 291 GENVANYI---KDLQKLSRL---FKDQVYPLLAFTROALNT---PDV---FGLVVLPL 337
DB 19 GDGVGNSYIEDNDSDSKADLISYFCQ---LTFQESVTKLQCPBELSSQIHISVLPM 73
QY 338 ELKLRIRL---LDVRSVLSAVCRDLFTASNDPLMRFLYLRDPDNTVR-VQDD 391
DB 74 EVMWYIFRWVSSDLDRSLSEQLSVCRGFYICARDEIWRACLKMGSSCIKLVYYS 133
QY 392 WKELYRKRIQRKSPKGRFVMLLPSSST---HTIPYPNPLPRPF 434
DB 134 WREWFLEL---PVRFDGVYISKTYIROEGSLDGFYRAMQVEY---RYIRFF 183

QY 435 PSSRLPGIIGGYDQRPFLPYVGDPLSLIPGSGETPSQFPLRPF 481
DB 184 PDGHV-----MMLTPEEPQSIYPRLRTR 207

RESULT 13
US-09-599-287A-2
Sequence 2; Application US/09599287A
Patent No. 6635446
GENERAL INFORMATION:
APPLICANT: Narayanaswamy Ramesh
APPLICANT: Ines M. Anton
APPLICANT: John H. Hartwig
APPLICANT: Raif S. Geba
TITLE OF INVENTION: WIP, A WASP-Associated Protein
FILE REFERENCE: 1242.1022-004
CURRENT APPLICATION NUMBER: US/09/599,287A
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: PCT/US98/27501
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/101,457
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/068,533
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 503
TYPE: PRT
ORGANISM: Human
US-09-599-287A-2

Query Match 4.3%; Score 117.5; DB 4; Length 503;
Best Local Similarity 33.1%; Pred. No. 0.023;
Matches 46; Conservative 9; Mismatches 41; Indels 43; Gaps 9;

QY 415 LPSSTHTIPYPNPLPRPFPSR---LPGIIGGYDQRPFLPYVGDPLSL---IP 466
DB 294 VSTR---PSADHRHLAPPPSRGPPPLPSSGN---DETPRLQNLISSTPLP 349
QY 467 GGET-----PSQPPPLPRPD---VGPLPGNPDI-----LPG----- 497
DB 350 SPSRSGPLPPPSRPPVVDPPFSGPLPPPSVNSGSTRALPATPOLPSRGVDS 409
QY 498 RGPNDRF-PPRPSGRP 514
DB 410 PRSGRPPPLPPDRPSAGAP 428

RESULT 14
US-09-598-287A-24
Sequence 24; Application US/09599287A
Patent No. 6635446
GENERAL INFORMATION:
APPLICANT: Narayanaswamy Ramesh
APPLICANT: Ines M. Anton
APPLICANT: John H. Hartwig
APPLICANT: Raif S. Geba
TITLE OF INVENTION: WIP, A WASP-Associated Protein
FILE REFERENCE: 1242.1022-004
CURRENT APPLICATION NUMBER: US/09/599,287A
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: PCT/US98/27501
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/101,457
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/068,533
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 507
TYPE: PRT

```
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translated WIP ORF No. 6635446 3
US-09-599-287A-24

Query Match
Best Local Similarity 4.2%; Score 117; DB 4; Length 507;
Best Local Similarity 32.9%; Pred. No. 0.026;
Matches 46; Conservative 9; Mismatches 41; Indels 44; Gaps 9;

QY 415 LPSTHTIPFYPNLHPPPPSSR-----LPPGILGGEYDORPLPYVGPPISSL--IP 466
DB 297 VPSFPR--PSAPHRPHLRPPPPSRGPPPLPSSSGN--DETPRLPQRNLSSSTPPLP 352
QY 467 GPGET-----PSQFPLRPRFDP--VGPLPGNP-----LPG-----497
DB 353 SPGRSGPLPPPPVPSERPPPPVDPGRSGPLPPPPVSRKSGTRALPAPQLPSSRGVD 412
QY 498 --RGPNDRF--PFRPSRGRP 514
DB 413 SPGRSGPLPPPPDRPSAGAP 432

RESULT 15
US-09-248-796A-19169
Sequence 19169, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248, 796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19169
LENGTH: 690
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-19169

Query Match
Best Local Similarity 4.1%; Score 112; DB 4; Length 690;
Best Local Similarity 20.0%; Pred. No. 0.13;
Matches 114; Conservative 76; Mismatches 189; Indels 192; Gaps 30;

QY 42 SNTREITLANKDPLTGDEET-----IASYGVISGDLICLLDIPAPIPST--DS 93
DB 166 SPPKASIALVVPDATEGTKESSIILALASLAKASGS-----NNETPPSSQSSSTNNNS 219
QY 94 EHSIQNNEOPLAT-----SSNQTSMODEQPSDSFQQAAGSG--VWDD-- 137
DB 220 NNSNSNSNSGSGNATNIIQLSALGNSNTGSASQPPSQOQYSYPOGGGQAGNDLL 279
QY 138 SML-----GPSQNFEAESIQDNAMAE-----159
DB 280 NMLQMOGGGPTGASPVASPVGSNEARGPFAEPRRRGRDNEYGSGOYGRNRSRSPKR 339
QY 160 GTGFYPSSEPMLCSESEVEGVSHLETTYQADCS-----DANDALIVLILHLMESGYIP 214
DB 340 GSNITWVRSP--SSSVQA--LQNMGNLRLQKQVNHGVQNTNG-----QVDQGFVP 387
QY 215 QGTEKALISPEKWKLSGVYKLQYMHPLCEGASATLTCVPLGNLIVNATIKI-----NN 269
DB 388 PVAMGELNLP-----GTPHYRPRTVQFDSF--IPQGVKVLSTLFLGVPFRM 435
QY 270 EIRSVKRLQLLP-----ESFICKERKGENVANIY--KDLQKLSRLFKDQLVYPL-----LA 318
DB 436 DERSLAQY--LRPYALIQVILNSEKKAFAVKYISRRRAEQVITSPNKDGLPLRTRWVG 494
QY 319 F-TROALNLPDVFGIVLPLEIKRIFRL-----346
```

```
DB 495 FGRPRCCNYQ--HGSIIPDQ-----RLTEADKNWIVHAQMGGTGQPIISGMVDEPD 546
QY 347 LDVRSVLSLAVCRDLFT--ASNDPLMRFLYLADFRNTYRVQDTWKE--LYRKHIQ 402
DB 547 IEIGGLSSKAKSKKMPNARSNGP-----KSNRGPBPDEEVKTTLLIPQDQ 595
QY 403 RKSPKGRFVMLPSTHTIPFYPNLHPPPPSSRLPPIIGGEYDORPLPYVGPPISS 462
DB 596 MTHGAQPCENTYLGSSV-----NPLQ-----GLFGNNPQOQOQPF--PPF 633
QY 463 SLIPPGETPSQFPLRFRFDPVGP--LPGFN 492
DB 634 PQPQPQPQPFMQPFAQFPQMPQOQPGOPGMN 664

Search completed: November 16, 2004, 07:13:13
Job time : 40 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:24:31 ; Search time 41 Seconds
(without alignments)

1225.004 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 522
Sequence: 1 MRURVRLKRTWPLEVPEPE.....DRPPRPSRGRPTDRLSPM 522

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR 79:*

1: PIR1:*\n2: PIR2:*\n3: PIR3:*\n4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	1.5	353	2	T21616
2	8	1.5	572	2	B84648
3	7	1.3	25	2	S22221
4	7	1.3	84	2	S76012
5	7	1.3	91	2	E86163
6	7	1.3	96	2	B75134
7	7	1.3	110	2	B55863
8	7	1.3	140	2	AH0243
9	7	1.3	150	2	S73394
10	7	1.3	160	1	AFAlAC
11	7	1.3	161	2	A31385
12	7	1.3	167	2	F97162
13	7	1.3	184	2	AG1489
14	7	1.3	188	2	T26741
15	7	1.3	196	2	B87271
16	7	1.3	216	2	AF2026
17	7	1.3	224	2	G72398
18	7	1.3	224	2	AH0875
19	7	1.3	229	2	F70800
20	7	1.3	238	2	T04166
21	7	1.3	243	2	D81804
22	7	1.3	246	2	T16371
23	7	1.3	257	2	A96033
24	7	1.3	261	2	A60404
25	7	1.3	269	2	F69541
26	7	1.3	269	2	D84312
27	7	1.3	273	2	T31506
28	7	1.3	278	2	B99415
29	7	1.3	291	2	S78602

30	7	1.3	292	2	A47125	transcription acti
31	7	1.3	299	2	B95939	probable spermidin
32	7	1.3	304	2	C73224	homoserine O-succin
33	7	1.3	307	2	A83123	probable transcrip
34	7	1.3	310	2	H82138	probable phosphati
35	7	1.3	311	2	A57223	pheromone receptor
36	7	1.3	315	2	B86342	probable cdc2 kina
37	7	1.3	316	2	A55975	galectin-8 - rat
38	7	1.3	316	2	A64384	transketolase (EC
39	7	1.3	323	2	T44256	thiamin biosynthes
40	7	1.3	324	1	UC4985	UTP-glucose-1-phos
41	7	1.3	338	2	S78045	erythrocyte membra
42	7	1.3	338	2	T02645	hypothetical prote
43	7	1.3	342	2	D86677	transcription regu
44	7	1.3	363	2	S31780	peroxidase (EC 1.1
45	7	1.3	376	2	C69813	RNA helicase homol
46	7	1.3	383	2	G84248	iron-binding prote
47	7	1.3	390	2	H83856	chorismate synthas
48	7	1.3	391	2	T32156	hypothetical prote
49	7	1.3	396	2	G71044	probable molybdopt
50	7	1.3	400	1	URX1A1	peptidylglycine mo
51	7	1.3	400	2	F75275	chromate transport
52	7	1.3	427	2	C83464	hypothetical prote
53	7	1.3	429	2	D78468	conserved hypotnet
54	7	1.3	433	2	H84826	hypothetical prote
55	7	1.3	436	2	H87329	conserved hypotnet
56	7	1.3	438	2	G96945	similar to ABC tra
57	7	1.3	446	2	S67437	Damage and replica
58	7	1.3	452	1	GMEBT	indole-3-glycerol-
59	7	1.3	452	2	AD0653	hypothetical prote
60	7	1.3	455	2	S80725	hypothetical prote
61	7	1.3	456	2	C86624	hypothetical prote
62	7	1.3	456	2	H72000	hypothetical prote
63	7	1.3	457	2	H84716	hypothetical prote
64	7	1.3	458	2	T31237	trab protein homol
65	7	1.3	468	2	AB0423	probable outer mem
66	7	1.3	495	2	S43294	bone morphogenetic
67	7	1.3	496	2	C85789	hypothetical prote
68	7	1.3	501	2	UC2347	growth/differentia
69	7	1.3	501	2	A55452	cartilage-derived
70	7	1.3	529	2	T20121	hypothetical prote
71	7	1.3	535	2	S74703	hypothetical prote
72	7	1.3	540	2	T49074	hypothetical prote
73	7	1.3	547	2	C66264	protein F319.5 [i
74	7	1.3	556	2	B64939	hypothetical prote
75	7	1.3	556	2	G90940	hypothetical prote
76	7	1.3	563	2	T04598	hypothetical prote
77	7	1.3	579	2	F83946	pyruvate synthase
78	7	1.3	585	1	A41292	glutamate decarbox
79	7	1.3	585	1	S38533	glutamate decarbox
80	7	1.3	585	1	JC4064	glutamate decarbox
81	7	1.3	594	2	B88956	protein ZK697.5 [i
82	7	1.3	594	2	F81113	protein ZK742.2 [i
83	7	1.3	602	1	S38111	amino acid transpo
84	7	1.3	606	2	S13526	hydrogenase (EC 1.
85	7	1.3	610	2	S56643	68k protein - phag
86	7	1.3	613	2	S19676	ferrous iron trans
87	7	1.3	617	2	FA7744	hypothetical prote
88	7	1.3	620	2	AE6504	transketolase (imp
89	7	1.3	670	2	A12223	hypothetical prote
90	7	1.3	681	2	F85062	novel antigen rece
91	7	1.3	684	2	S60266	protein F5011.8 [i
92	7	1.3	733	2	C66258	outer layer protei
93	7	1.3	736	1	VPXRPC	amine oxidase (cop
94	7	1.3	751	2	A54053	hypothetical prote
95	7	1.3	758	2	D71072	outer membrane ass
96	7	1.3	839	2	H97758	protein kinase hom
97	7	1.3	878	2	T08559	hypothetical prote
98	7	1.3	880	2	T44477	CES1 protein - yea
99	7	1.3	915	2	S54485	peptidylglycine mo
100	7	1.3	935	2	S17855	

ALIGNMENTS

RESULT 1

hypothetical protein F32A11.3 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T21616

R/Type, R. submitted to the EMBL Data Library, November 1996

A/Reference number: Z19450

A/Accession: T21616

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-553 <WILL>

A/Cross-references: UNIPROT:O62197; EMBL:Z81521; PTDN:CA804225.1; GSPDB:GN00020; CESP:F3

A/Experimental source: clone F32A11

C/Genetics:

A/Gene: CESP:F32A11.3

A/Map position: 2

A/Introns: 21/1; 221/3; 298/3

Query Match 1.5%; Score 8; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 RSVLSLSA 357
DB 53 RSVLSLSA 60

RESULT 2

hypothetical protein At2g25420 [imported] - *Arabidopsis thaliana*

C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: B84648

R/Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Mayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A/Reference number: A84420; MUID:20083487; PMID:1061297

A/Accession: B84648

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-572 <STO>

A/Cross-references: UNIPROT:Q9SKK7; GB:AEO02093; NID:g4432854; PTDN:AAD20702.1; GSPDB:GN

C/Genetics:

A/Gene: At2g25420

A/Map position: 2

Query Match 1.5%; Score 8; DB 2; Length 572;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 DLICILQ 79
DB 96 DLICILQ 103

RESULT 3

peroxidase (EC 1.11.1.7) - imperfect fungus (*Archiomyces ramosus*) (fragment)

C/Species: *Archiomyces ramosus*

C/Date: 12-Feb-1998 #sequence_revision 17-Apr-1998 #text_change 12-Jul-2004

C/Accession: S22221

R/Kjalk, M.; Andersen, M.B.; Schneider, P.; Christensen, B.; Schuelein, M.; Welinder, K.

Biochim. Biophys. Acta 1120, 248-256, 1992

A/Title: Comparison of structure and activities of peroxidases from *Coprinus cinereus*, C

A/Reference number: S21746; MUID:92247803; PMID:1576150

A/Accession: S22221

A/Molecule type: protein
A/Residues: 1-25 <KJA>
C/Superfamily: Peroxidase
C/Keywords: blocked amino end; glycoprotein; oxidoreductase

Query Match 1.3%; Score 7; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
DB 10 SLIPPG 16

RESULT 4

hypothetical protein - *Synechocystis* sp. (strain PCC 6803)

C/Species: *Synechocystis* sp.

A/Variety: PCC 6803

C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: S76012

R/Kaneke, T.; Satoh, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

S.

A/Reference number: S74322; MUID:97061201; PMID:8905231

A/Accession: S76012

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-84 <KAN>

A/Cross-references: UNIPROT:P74781; EMBL:D64006; GB:AB001339; NID:g1001291; PTDN:BA10855

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Superfamily: conserved hypothetical protein H10721

Query Match 1.3%; Score 7; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 QVPHSL 184
DB 49 QVPHSL 55

RESULT 5

protein F15K9.18 [imported] - *Arabidopsis thaliana*

C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: E86163

R/Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.T.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Xu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: E86163

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-91 <STO>

A/Cross-references: UNIPROT:Q9ZVS3; GB:AF005172; NID:g3850586; PTDN:AACT2126.1; GSPDB:GN

C/Genetics:

A/Gene: F15K9.18

A/Map position: 1

Query Match 1.3%; Score 7; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 LIAFTRO 322
 |||||
 Db 80 LIAFTRO 86

RESULT 6

B55863
 hypothetical protein PAB7218 - *Pyrococcus abyssi* (strain Orsay)
 C/Species: *Pyrococcus abyssi*
 C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C/Accession: B55134
 R/anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A/Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru
 A/Reference number: A75001
 A/Accession: B55134
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-96 <KIM>
 A/Cross-references: UNIPROT:Q9V0B7; GB:AJ248285; GB:AL096836; NID:G5458067; PIDN:CAB4978
 A/Experimental source: strain Orsay
 C/Genetics:
 A/Gene: PAB7218

Query Match

1.3%; Score 7; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 NDALIVL 202
 |||||
 Db 63 NDALIVL 69

RESULT 7

B55863
 excisionase - *Streptococcus pneumoniae* transposon Tns252
 C/Species: *Streptococcus pneumoniae*
 C/Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
 C/Accession: B55863
 R/Kilic, A.O.; Vijayakumar, M.N.; Al-Khalidi, S.F.
 J. Bacteriol. 176, 5145-5150, 1994
 A/Title: Identification and nucleotide sequence analysis of a transfer-related region in
 A/Reference number: A55863; MUID:94327488; PMID:8051031
 A/Accession: B55863
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-110 <KIL>
 A/Cross-references: UNIPROT:Q54878; GB:U29324; NID:G4063727; PIDN:AAC98429.1; PID:G46002
 C/Superfamily: *Streptococcus pneumoniae* transposon Tns252 excisionase

Query Match

1.3%; Score 7; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 YKDPITG 58
 |||||
 Db 21 YKDPITG 27

RESULT 8

AH0243
 4-carboxymuconolactone decarboxylase (EC 4.1.1.44) [Imported] - *Yersinia pestis* (strain
 C/Species: *Yersinia pestis*
 C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C/Accession: AH0243
 R/Parikhilli, U.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Pentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
 Nature 413, 523-527, 2001
 A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A/Reference number: AB0001; MUID:21470413; PMID:11586360
 A/Accession: AH0243

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-140 <KIR>
 A/Cross-references: UNIPROT:Q8ZEZ7; GB:AL590842; PIDN:CAC90812.1; PID:G15980013; GSPDB:GT
 C/Genetics:
 A/Gene: YPO1999
 C/Keywords: carbon-carbon lyase; carboxy-lyase

Query Match

1.3%; Score 7; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRSRLRL 32
 |||||
 Db 92 LRSRLRL 98

RESULT 9

S73394
 hypothetical protein R02_orf150 - *Mycoplasma pneumoniae* (strain ATCC 29342)
 C/Species: *Mycoplasma pneumoniae*
 A/Variety: ATCC 29342
 C/Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S73394
 R/Himmelreich, R.; Hilbert, H.; Plagens, H.; Pitkl, E.; Li, B.C.; Herrmann, R.
 Nucleic Acids Res. 24, 4420-4449, 1996
 A/Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*.
 A/Reference number: S73327; MUID:97105885; PMID:8948633
 A/Accession: S73394
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-150 <HLV>
 A/Cross-references: UNIPROT:P75606; EMBL:AE000009; GB:U00089; NID:G1673720; PIDN:AAB95714
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C/Genetics:
 A/genetic code: SGC3

Query Match

1.3%; Score 7; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 DVFGILV 334
 |||||
 Db 94 DVFGILV 100

RESULT 10

AER1AC
 allophycocyanin alpha chain - *Anabaena cylindrica*
 C/Species: *Anabaena cylindrica*
 C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C/Accession: A24224
 R/Mimami, Y.; Yamada, F.; Hase, T.; Matsubara, H.; Murakami, A.; Fujita, Y.; Takao, T.; S
 FEBS Lett. 191, 216-220, 1985
 A/Title: Amino acid sequences of allophycocyanin alpha- and beta-subunits isolated from
 A/Reference number: A91349
 A/Accession: A24224
 A/Molecule type: protein
 A/Residues: 1-160 <MIN>
 A/Cross-references: UNIPROT:P07325
 C/Comment: This protein is a common component of light-gathering protein complexes calle
 C/Superfamily: phycocyanin
 C/Keywords: chromoprotein; photosynthesis; phycocyanobilin
 F/80/Binding site: phycocyanobilin (Cys) (covalent) #status experimental

Query Match

1.3%; Score 7; DB 1; Length 160;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YGIVSGD 72
 |||||
 Db 93 YGIVSGD 99

RESULT 11
A:Species: Calothrix sp.
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jun-1999
C:Accession: A31385; A30764
R:Howard, J.; Capuano, V.; Coursin, T.; Tandeau de Marsac, N.
J. Bacteriol. 170..5512-5521, 1988
A:Title: Genes encoding core components of the phycobilisome in the cyanobacterium Calot
A:Reference number: A31890; MUID:85053869; PMID:2461338
A:Accession: A31385
A:Molecule type: DNA
A:Residues: 1-161 <HOU>
A:Cross-references: GB:M20806; NID:g148538; PIDN:AAA24874.1; PID:g148540
C:Superfamily: phycocyanin
C:Keywords: chromoprotein; photosynthesis; phycocyanobilin
F:81/Binding site: phycocyanobilin (Cys) (covalent) #status predicted

Query Match 1.3%; Score 7; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YGIVSGD 72
DB 94 YGIVSGD 100

RESULT 12
F97162
hypothetical protein CAC2131 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: F97162
R:Noelling, J.; Breton, G.; Meichen, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.
J. Bacteriol. 183. 4823-4838, 2001
J. Bacteriol. 183. 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A:Reference number: A96900; MUID:21359325; PMID:21539325
A:Accession: F97162
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-167 <KTR>
A:Cross-references: UNIPROT:Q97H82; GB:AE001437; PIDN:AAK60089.1; PID:g15025122; GSPDB:G
C:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2131

Query Match 1.3%; Score 7; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 LKRIFR 345
DB 103 LKRIFR 109

RESULT 13
AG1489
hypothetical protein lin0455 [imported] - Listeria innocua (strain C1p11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG1489
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duhand, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feih, H.
Science 294. 849-852, 2001
A:Authors: Kretz, U.; Kunz, M.; Kunst, F.; Kurapkac, G.; Madeno, E.; Maitournam, A.; Ma
Ok, C.; Schuener, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.
A:Title: Comparative genomes of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1489
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-184 <GLA>
A:Cross-references: UNIPROT:Q92EK4; GB:AL592022; PIDN:CAC95687.1; PID:g16412896; GSPDB:G
A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: lin0455

Query Match 1.3%; Score 7; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 VLPLEL 339
DB 59 VLPLEL 65

RESULT 14
T26741
hypothetical protein Y39A1A.21 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26741
R:Wall, M.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z20257
A:Accession: T26741
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-188 <MIL>
A:Cross-references: UNIPROT:Q9XX11; EMBL:AL031633; PIDN:CAA21030.1; GSPDB:GN00021; CESP:Y
C:Experimental source: clone Y39A1A
C:Genetics:
A:Gene: CBSP:Y39A1A.21
A:Map position: 3
A:Introns: 76/3; 114/2; 171/3

Query Match 1.3%; Score 7; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 SLATSSN 111
DB 53 SLATSSN 59

RESULT 15
B87271
general secretion pathway protein J [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: B87271
R:Nierman, W.C.; Feldlynn, T.V.; Paulsen, I.T.; Neilson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Lamb, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolome
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98. 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; MUID:21173698; PMID:11259647
A:Accession: B87271
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-196 <STO>
A:Cross-references: UNIPROT:Q9ABP7; GB:AE005673; NID:g13421298; PIDN:AAK22166.1; GSPDB:G
C:Superfamily: secretion protein xcpM

Query Match 1.3%; Score 7; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 315 PULAFTR 321
DB 89 PULAFTR 95

RESULT 16
AF2026
hypothetical protein all1764 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF2026
R:Kanehiko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriyuchi, Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA: Res. 6, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2026
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-216 <KUR>
A:Cross-references: UNIPROT:Q8WY82; GB:BA000019; PIDN:BA073463.1; PID:G17130854; GSPDB:C
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1764

Query Match 1.3%; Score 7; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 DSFGQA 128
Db 103 DSFGQA 109

RESULT 17
G72398
hypothetical protein TM0246 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: G72398
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: G72398
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <ARN>
A:Cross-references: UNIPROT:Q9WY88; GB:AE001708; GB:AE000512; NID:G4980740; PIDN:AAD3533
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0246
C:Superfamily: Thermotoga maritima hypothetical protein TM0246

Query Match 1.3%; Score 7; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 KDPLTGD 59
Db 50 KDPLTGD 56

RESULT 18
AH0875
probable membrane protein SRY3231 [imported] - Salmonella enterica subsp. enterica serov
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH0875
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, th, T.; Conneron, P.; Courtin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <PAR>
A:Cross-references: GB:AL513382; PIDN:CA002904.1; PID:G1650457; GSPDB:GN00176
C:Genetics:
A:Gene: SRY3231

Query Match 1.3%; Score 7; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 437 SRLPPI 443
Db 108 SRLPPI 114

RESULT 19
F70800
probable transport system permease protein - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: F70800
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Galloway, S.; Hamilton, N.; Holtz, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sultson, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70800
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-229 <COL>
A:Cross-references: UNIPROT:O69723; GB:AL022121; GB:AL23456; NID:G3261559; PIDN:CAA1807
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: proV
C:Superfamily: ABC transporter permease protein

Query Match 1.3%; Score 7; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 HRLSL 35
Db 18 HRLSL 24

RESULT 20
T04166
thaumatin-like protein - rice
C:Species: Oryza sativa (rice)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04166
R:Cole, K.C.; Velazhahan, R.; Anuratha, C.S.; Muthukrishnan, S.
submitted to the EMBL Data Library, November 1996
A:Description: Induction of thaumatin-like proteins (TLPs) in Rhizoctonia solani - infecte
A:Reference number: Z15250
A:Accession: T04166
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-238 <COL>
A:Cross-references: UNIPROT:O04364; EMBL:U77657; NID:G2062388; PIDN:AB53368.1; PID:G206;
C:Superfamily: thaumatin I

Query Match 1.3%; Score 7; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A/Reference number: A69250; MUID:98049343; PMID:9389475
A/Accession: F69541
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-269 <XLE>
A/Cross-references: UNIPROT:Q27950; GB:AE000943; GB:AE000782; NID:G2689266; PIDN:AA8891
C/Superfamily: spermidine synthase

Query Match 1.3%; Score 7; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 443 IIGGEYD 449
DB 222 IIGGEYD 228

RESULT 26
D84312
sulfate transport system permease protein [imported] - Halobacterium sp. NRC-1
C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: D84312
R/NG: W.V.; Kennedy, S.P.; Maharez, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Jaeky, S.;
Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jaldic
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A/Title: Genome sequence of Halobacterium species NRC-1.
A/Reference number: A84160; MUID:20504483; PMID:11016950
A/Accession: D84312
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-269 <SNO>
A/Cross-references: UNIPROT:Q9HPK3; GB:AE004437; NID:G10581074; PIDN:AA319864.1; GSPDB:C
C/Genetics:
A/Gene: cyst2
C/Superfamily: maltose transport protein malG

Query Match 1.3%; Score 7; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 331 GLVVLPL 337
DB 95 GLVVLPL 101

RESULT 27
T31506
hypothetical protein Y116A8C.40 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T31506
R/McMurray, A.
submitted to the EMBL Data Library, October 1999
A/Reference number: Z21041
A/Accession: T31506
A/Status: preliminary; translated from GB/EMBL/DD347
A/Molecule type: DNA
A/Residues: 1-273 <WIL>
A/Cross-references: UNIPROT:Q9J2T7; EMBL:AL117204; PIDN:CAB55140.1; CESP:Y116A8C.40
A/Experimental source: clone Y116A8C
C/Genetics:
A/Gene: CESP:Y116A8C.40
A/Intons: 38/2; 83/2; 130/3; 236/1

Query Match 1.3%; Score 7; DB 2; Length 273;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 351 SVLSLSA 357

DB 9 SVLSLSA 15

RESULT 28
B99415
hypothetical protein cutB-1 [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: B99415
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-Y
Jong, I.; Jeffries, A.C.; Kozera, C.D.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrest, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A89139
A/Accession: B99415
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-278 <KUR>
A/Cross-references: UNIPROT:Q97W13; GB:AE006641; NID:G13815737; PIDN:AAK42577.1; GSPDB:G
C/Genetics:
A/Gene: cutB-1
C/Superfamily: carbon monoxide dehydrogenase medium chain

Query Match 1.3%; Score 7; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 339 LKLRIFR 345
DB 40 LKLRIFR 46

RESULT 29
S78602
peroxidase (EC 1.11.1.7) - inky cap (Coprinus macrochrous) (fragments)
C/Species: Coprinus macrochrous
C/Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 12-Jul-2004
C/Accession: S78602; S22220
R/Baunsgaard, L.; Dalboe, H.; Houen, G.; Rasmussen, E.M.; Welinder, K.G.
Eur. J. Biochem. 213, 605-611, 1993
A/Title: Amino acid sequence of Coprinus macrochrous peroxidase and cDNA sequence encodir
A/Reference number: S30357; MUID:93238741; PMID:8477731
A/Accession: S78602
A/Molecule type: protein
A/Residues: 1-17;18-27;28-59;60-138;139-141;142-256;257-281;282-287;288-291 <BAU>
R/Kjaer, M.; Andersen, M.B.; Schneider, P.; Christensen, B.; Schneider, M.; Welinder, K.
Biochim. Biophys. Acta 1120, 248-256, 1992
A/Title: Comparison of structure and activities of peroxidases from Coprinus cinereus, C
A/Reference number: S21746; MUID:92247803; PMID:1576150
A/Accession: S22220
A/Molecule type: protein
A/Residues: 97-121 <KJA>
C/Superfamily: peroxidase
C/Keywords: blocked amino end; glycoprotein; oxidoreductase; pyroglyutamic acid
F/Modified site: pyroliodone carboxylic acid (Gln) #status experimental

Query Match 1.3%; Score 7; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 463 SLIRPG 469
DB 106 SLIRPG 112

RESULT 30
A47125
transcription activator of cholera toxin toxR - Vibrio parahaemolyticus (strain A03815)
C/Species: Vibrio parahaemolyticus
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: A47125

R./Lin, Z.; Kumagai, K.; Baba, K.; Mekalanos, J.J.; Nishibuchi, M.
J. Bacteriol. 175, 3844-3855, 1993
A:Title: Vibrio parahaemolyticus has a homolog of the Vibrio cholerae toxS operon that
A:Reference number: A47125; MUID:93285998; PMID:8509337
A:Accession: A47125
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292 <LIN>
A:Cross-references: UNIPROT:Q05938; GB:L11929; NID:g295440; PIDN:AAA27576.1; PID:g295441
A:Notes: authors translated the codon AGC for residue 28 as Thr
C:Genetics:
A:Gene: toxS
C:Keywords: DNA binding; transcription regulation; transmembrane protein

Query Match 1.3%; Score 7; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 PSLATSS 110
DB 147 PSLATSS 153

RESULT 31
B95939
Probable spermidine/putrescine ABC transporter permease protein potB [imported] - Sinorhizobium meliloti
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95939
R.Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb P_{SYMB} megaplasmid from the N₂-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: B95939
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <KTR>
A:Cross-references: UNIPROT:Q92VD0; GB:AL591985; PIDN:CAC49178.1; PID:g15140663; GSPDB:C
R:Experimental source: strain 1021, megaplasmid SYMB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.;
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: potB; SMD21274
A:Genome: plasmid
C:Superfamily: spermidine/putrescine transport system permease protein potB

Query Match 1.3%; Score 7; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 331 GLVVLPL 337
DB 121 GLVVLPL 127

RESULT 32
C72324
homoserine O-succinyltransferase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: C72324
R.Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.W.; Stewart, A.W.; Cotton, M.D.; Pratt, W.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72324
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <ARN>
A:Cross-references: UNIPROT:Q9WY3; GB:AE001753; GB:AE000512; NID:g4981397; PIDN:AAD3596;
C:Genetics:
A:Experimental source: strain MSB8
A:Gene: TM0881
C:Superfamily: homoserine O-succinyltransferase

Query Match 1.3%; Score 7; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 KLSGYK 235
DB 163 KLSGYK 169

RESULT 33
A83123
probable transcription regulator PA4174 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: A83123
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Er
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latib, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83123
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-307 <STO>
A:Cross-references: UNIPROT:Q9HWK7; GB:AE004834; GB:AE004091; NID:g9950382; PIDN:AA07561
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA4174

Query Match 1.3%; Score 7; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RLVRLL 8
DB 43 RLVRLL 49

RESULT 34
H82138
Probable phosphatidate cytidyllyltransferase VC1936 [imported] - Vibrio cholerae (strain
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82138
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: H82138
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <HEI>
A:Cross-references: UNIPROT:Q9KOR2; GB:AE004269; GB:AE003852; NID:g9656466; PIDN:AAF5508;
C:Genetics:
A:Experimental source: serogroup O1, strain N16961, biotype El Tor
A:Gene: VC1936
A:Map position: 1

Query Match 1.3%; Score 7; DB 2; Length 310;

Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 LEIKLRI 343
DB 39 LEIKLRI 45

RESULT 35

A57223
Pheromone receptor VN3 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: A57223
R/Dulac, C.; Axel, R.
Cell 83, 195-206, 1995
A/Title: A novel family of genes encoding putative pheromone receptors in mammals.
A/Reference number: A57223; MUID:96028094; PMID:7585937
A/Accession: A57223
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-311 <RES>
A/Cross-references: UNIPROT:Q62852; EMBL:U36895; NID:g1055247; PIND:AA652284.1; PID:g105
C/Superfamily: pheromone receptor VN3t

Query Match 1.3%; Score 7; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 LIHLML 208
DB 58 LIHLML 64

RESULT 36

B86342
Probable cdcc2 kinase (imported) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: B86342
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A61411; MUID:21016719; PMID:11130712
A/Accession: B86342
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-315 <STO>
A/Cross-references: UNIPROT:Q98YPA; GB:AF005172; NID:g4836894; PIND:AA30597.1; GSPDB:GN
C/Genetics: 1
A/Map position: 1
C/Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 1.3%; Score 7; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 LRIFRL 347
DB 234 LRIFRL 240

RESULT 37

A55975
Galectin-8 - rat
C/Species: Rattus norvegicus (Norway rat)

C/Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C/Accession: A55975
R/Hadadi, Y.R.; Paz, K.; Dekel, R.; Mestrovic, T.; Accilli, D.; Zick, Y.
J. Biol. Chem. 270, 3447-3453, 1995
A/Title: Galectin-8. A new rat lectin, related to galectin-4.
A/Reference number: A55975; MUID:95155445; PMID:7852431
A/Accession: A55975
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-316 <HAD>
A/Cross-references: UNIPROT:Q62665; GB:U09824; NID:g717031; PIND:AA66359.1; PID:g717032
C/Superfamily: lactose-binding lectin L-36

Query Match 1.3%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 RLIDYRS 351
DB 309 RLIDYRS 315

RESULT 38

G64384
transketolase (EC 2.2.1.1) - Methanococcus jannaschii
C/Species: Methanococcus jannaschii
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 12-Jul-2004
C/Accession: G64384
R/Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.; Reich, C.I.; Overbeek, R.; Kirsch, E.P.; Weinstock, K.G.; Merrick, J.M.; Glöck, A.; Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A/Reference number: A64300; MUID:96337999; PMID:8688087
A/Accession: G64384
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-316 <BU>
A/Cross-references: UNIPROT:Q58092; GB:U67515; GB:L77117; NID:g1591390; PIND:AA98674.1; C/Genetics: 1
A/Map position: REV606237-605287
C/Superfamily: transketolase, C-terminal subunit
C/Keywords: transferase

Query Match 1.3%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 KLSGVYK 235
DB 3 KLSGVYK 9

RESULT 39

T44256
thiamin biosynthesis protein thig [similarity] - Rhizobium etli plasmid b
C/Species: Rhizobium etli
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 24-Oct-2000
C/Accession: T44256
R/Miranda-Rios, J.; Morena, C.; Taboada, H.; Davalos, A.; Encarnacion, S.; Mora, J.; Sobe J. Bacteriol. 179, 6887-6893, 1997
A/Title: Expression of thiamin biosynthetic genes (thiCOGE) and production of symbiotic t
A/Reference number: Z22737; MUID:98037482; PMID:9371431
A/Accession: T44256
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-323 <MIR>
A/Cross-references: EMBL:AF004408; NID:g2627325; PIND:AA645974.1; PID:g2627328
A/Experimental source: strain CE3
C/Genetics: 1
A/cene: thig
A/genome: plasmid b

C:Function:
A:Description: involved in the biosynthesis of the thiazole moiety of thiamin
C:Superfamily: thiamin biosynthesis protein thig

Query Match 1.3%; Score 7; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 327 PDVFGLV 333
Db 174 PDVFGLV 180

RESULT 40

UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) [validated] - Xanthomonas campestris
N:Alternate names: udp-glucose pyrophosphorylase
C:Species: Xanthomonas campestris
C>Date: 15-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004

A:Accession: U04985
R:Wei, C.L.; Lin, N.T.; Wang, S.F.; Tseng, Y.H.
Biochem. Biophys. Res. Commun. 226, 607-612, 1996
A:Title: The gene encoding UDP-glucose pyrophosphorylase is required for the synthesis of
A:Reference number: U04985; MUID:96428562; PMID:8831665
A:Accession: U04985

A:Molecule type: DNA
A:Residues: 1-324 <WEI>
A:Cross-references: UNIPROT:P74969; GB:U65532; NID:G1628574; PIDN:AA017376.1; PID:G16285
C:Genetics:
A:Map position: Xc17
A:Function:
A:Description: catalyzes the reaction of UTP and glucose-1-phosphate to form UDP-1-glucose
C:Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase
C:Keywords: nucleotidyltransferase

Query Match 1.3%; Score 7; DB 1; Length 324;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 ASYGIVS 70
Db 171 ASYGIVS 177

RESULT 41

S78045
erythrocyte membrane-associated antigen (clone pPF 64) - Plasmodium falciparum (fragment
C:Species: Plasmodium falciparum
C>Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

A:Accession: S78045
R:Kun, J.; Hesselbach, J.; Scherf, M.; Scherf, A.; Gysin, J.; Mattei, D.; Pereira da
Res. Immunol. 142, 199-210, 1991
A:Title: Cloning and expression of genomic DNA sequences coding for putative erythrocyte
A:Reference number: S23684; MUID:91376328; PMID:1896607
A:Accession: S78045

A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-338 <KUN>
A:Cross-references: UNIPROT:Q06166

R:Kun, J.
submitted to the EMBL Data Library, May 1990
A:Reference number: S23690

A:Accession: S23690
A:Molecule type: DNA
A:Residues: 1-104 <KUN>
A:Cross-references: EMBL:X53021
C:Superfamily: ring-infected erythrocyte surface antigen; dnas amino-terminal homology
C:Keywords: surface antigen

Query Match 1.3%; Score 7; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 288 EXLGENV 294
Db 284 EXLGENV 290

RESULT 42

T02645
hypothetical protein At2g26900 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F12C20.6
C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
A:Accession: T02645
R:Rounsley, S.D.; Rounsley, C.M.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sy
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence.
A:Reference number: T14685

A:Accession: T02645
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-338 <ROU>
A:Cross-references: UNIPROT:O81017; EMBL:AC005168; NID:G3426033; PID:G3426051
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
enus, D.; Nielsen, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A04420; MUID:20083487; PMID:10617157

A:Accession: G94666
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-338 <STO>
A:Cross-references: GB:AB002093; NID:G3426051; PIDN:AA032250.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g26900; F12C20.6
A:Map position: 2
A:introns: 22/2; 61/3; 99/3; 120/3; 163/2; 190/3; 208/1; 240/3; 293/3

Query Match 1.3%; Score 7; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 514 PTGRLS 520
Db 9 PTGRLS 15

RESULT 43

D86677
transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

A:Accession: D86677
R:Boletín, A.; Winkler, P.; Mauger, S.; Tallon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86677

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-342 <STO>
A:Cross-references: UNIPROT:O9CIE3; GB:AB005176; PID:G12723295; PIDN:AA04518.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yecE

Query Match 1.3%; Score 7; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 GDETLA 64
Db 314 GDETLA 320

RESULT 44

531780
peroxidase (EC 1.11.1.7) precursor - inky cap (*Coprinus cinereus*)

C/Species: *Coprinus cinereus*

C/Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 12-Jul-2004

C/Accession: S31780; S30357; S21746

R/Baunsgaard, L.; Wind, J.; Dalboge, H.

submitted to the EMBL Data Library, January 1993

A/Reference number: S31780

A/Accession: S31780

A/Molecule type: DNA

A/Residues: 1-363 <BAU>

A/Cross-references: UNIPROT:Q12575; EMBL:X70789; NID:92538; PIDN:CAA50060.1; PID:92539

A/Experimental source: strain IFO 8371

R/Baunsgaard, L.; Dalboge, H.; Houen, G.; Rasmussen, E.M.; Welinder, K.G.

Eur. J. Biochem. 213, 605-611, 1993

A/Title: Amino acid sequence of *Coprinus macrohizus* peroxidase and cDNA sequence encoded

A/Reference number: S30357; MUID:93238741; PMID:8477731

A/Accession: S30357

A/Molecule type: mRNA

A/Residues: 1-118, 'V', 120-363 <BAU>

A/Cross-references: EMBL:X69457; NID:92540; PIDN:CAA49216.1; PID:92541

A/Experimental source: strain IFO 8371

R/Kjalke, M.; Andersen, M.B.; Schneider, P.; Christensen, B.; Schueler, M.; Welinder, K.

Biochim. Biophys. Acta 1120, 248-256, 1992

A/Title: Comparison of structure and activities of peroxidases from *Coprinus cinereus*, C

A/Reference number: S21746; MUID:92247803; PMID:1576150

A/Accession: S21746

A/Molecule type: protein

A/Residues: 161, 'X', 163-185 <KXA>

A/Experimental source: strain IFO 30114

C/Genetics:

A/Insertions: 41/3; 56/2; 63/1; 68/3; 71/3; 91/2; 96/1; 110/1; 136/2; 216/3; 234/3; 283/3;

C/Keywords: blocked amino end; glycoprotein; oxidoreductase; pyroglyutamic acid

F/1-20/Domin: signal sequence #status predicted <SIG>

F/21-363/Product: peroxidase #status predicted <MAY>

F/21/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen

F/162/Binding site: carboxylate (Asn) (covalent) #status predicted

F/351/Binding site: carboxylate (Thr) (covalent) #status predicted

F/358/Binding site: carboxylate (Ser) (covalent) #status predicted

Query Match 1.3%; Score 7; DB 2; Length 363;

Best Local Similarity 100.0%; Pred. No. 98;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 170 SLIPGP 176

RESULT 45

69813
RNA helicase homolog yfml - *Bacillus subtilis*

C/Species: *Bacillus subtilis*

C/Date: 05-Dec-1997 #sequence revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: C69813

R/Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C./ Bron, S.; Brulliet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Harold, D.; Fritze, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Gallier

tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hult, K.F.

Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A/Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akerchi, M.; Tamacchini, A.; Tanaka, T.; Terstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipit, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Zumbstein, E.

A/Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: C69813

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-376 <KUN>

A/Cross-references: UNIPROT:Q34750; GB:Z99108; GB:AL009126; NID:62633055; PIDN:CA812572.1

A/Experimental source: strain 168

C/Genetics:

A/Supernatural: translation initiation factor eIF-4A

C/Keywords: ATP; nucleotide binding; P-loop

F/48-55/Region: nucleotide-binding motif A (P-loop)

F/149-154/Region: nucleotide-binding motif B

F/153-156/Region: DEAD motif

Query Match 1.3%; Score 7; DB 2; Length 376;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 233 LQKSLR 239

RESULT 46

84248
iron-binding protein [imported] - *Halobacterium* sp. NRC-1

C/Species: *Halobacterium* sp. NRC-1

C/Date: 02-Feb-2001 #sequence revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: G84248

R/Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.

; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo

Jung, K.H.; Alm, M.; Freilich, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A/Authors: Hou, S.; Daniels, C.O.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A/Title: Genomic sequence of *Halobacterium* species NRC-1.

A/Reference number: A84160; MUID:20504483; PMID:11016950

A/Accession: G84248

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-383 <STO>

A/Cross-references: UNIPROT:Q9HRC4; GB:A8004437; NID:910580483; PIDN:AA619355.1; GSPDB:G

C/Genetics:

A/Genes: ibp

Query Match 1.3%; Score 7; DB 2; Length 383;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 483 DVGPLP 489

345 DVGPLP 351

RESULT 47

88856
chorismate synthase aroF [imported] - *Bacillus halodurans* (strain C-125)

C/Species: *Bacillus halodurans*

C/Date: 01-Dec-2000 #sequence revision 01-Dec-2000 #text_change 09-Jul-2004

C/Accession: H88856

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and c

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: H88856

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-390 <STO>

A/Cross-references: UNIPROT:Q9KCB7; GB:AP001512; GB:BA000004; NID:910174030; PIDN:BA8053;

A/Experimental source: strain C-125

C/Genetics:

A/Genes: aroF

C:Superfamily: chorismate synthase

Query Match 1.3%; Score 7; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 PLTGDEE 61
|||
Db 92 PLTGDEE 98

RESULT 48

T32156
hypothetical protein C29G2.5 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T32156

R:Beck, C.; Wamsley, P.

submitted to the EMBL Data Library, September 1997

A:Description: The sequence of *C. elegans* cosmid C29G2.

A:Reference number: Z21128

A:Accession: T32156

A:Status: preliminary; translated from GB/EMBL/DDB

A:Molecule type: DNA

A:Residues: 1-391 <BEC>

A:Cross-references: UNIPROT:O16884; EMBL:AF022969; PDB:AA69894.1; GSPDB:GN00023; CESP:

A:Experimental source: strain Bristol N2; clone C29G2

C:Genetics:

A:Gene: CESP:C29G2.5

A:Map position: 5

A:introns: 8/1; 84/1; 113/1; 153/3; 175/3; 316/3

Query Match 1.3%; Score 7; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 ISSLIPG 467
|||
Db 211 ISSLIPG 217

RESULT 49

G71044

probable molybdopterin biosynthesis moeA protein - *Pyrococcus horikoshii*

C:Species: *Pyrococcus horikoshii*

C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004

C:Accession: G71044

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki,

M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5; 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: G71044

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-396 <KAN>

A:Cross-references: UNIPROT:O59354; GB:AP000006; NID:G3236133; PDB:BAA30759.1; PID:G325

A:Experimental source: strain OT3

A>Note: this accession replaces an interim accession for a sequence replaced by Genbank

C:Genetics:

A:Gene: PH1547

C:Superfamily: molybdenum cofactor biosynthesis protein, MoeA type

Query Match 1.3%; Score 7; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 ILQDDIP 83
|||
Db 331 ILQDDIP 337

RESULT 50

URK1A1

peptidylglycine monooxygenase (EC 1.14.17.3) I precursor - African clawed frog

N:Alternate names: C-terminal alpha-amidating enzyme AE-I; peptidyl alpha-amidating enzy

C:Species: *Xenopus laevis* (African clawed frog)

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C:Accession: A29726; S54374

R:Minano, K.; Ohnuye, K.; Wada, Y.; Fuchimura, K.; Tanaka, S.; Matsuo, H.

Biochem. Biophys. Res. Commun. 148; 546-552, 1987

A:Title: Cloning and sequence of cDNA encoding a peptidyl C-terminal alpha-amidating enzy

A:Reference number: A29726; MUID:88076923; PMID:3689360

A:Accession: A29726

A:Molecule type: mRNA

A:Residues: 1-400 <MTZ>

A:Cross-references: UNIPROT:P08478; GB:M33461

A:Experimental source: skin

A:Accession: S54374

A:Molecule type: Protein

A:Residues: 38-51;82-96;146-153;174-178;189-193;237-250;256-288;359-381 <MTW>

A:Experimental source: skin

C:Function: catalyzes oxidation of peptidylglycine to the corresponding peptidyl(2-hy

A:Description: catalyzes oxidation of peptidylglycine to the corresponding peptidyl(2-hy

A:Note: C-terminal alpha-amide structure is essential for the biological activity of man

C:Superfamily: peptidylglycine monooxygenase I; peptidylglycine monooxygenase I homology

C:Keywords: copper; monooxygenase; oxidoreductase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-37/Domain: propeptide #status predicted <PRO>

F:38-381/Product: peptidylglycine monooxygenase I #status experimental <MAT>

F:131-342/Domain: peptidylglycine monooxygenase I homology <PGM>

F:382-400/Domain: carboxyl-terminal propeptide #status predicted <CTP>

Query Match 1.3%; Score 7; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 NIPSTSD 92
|||
Db 111 NIPSTSD 117

RESULT 51

F75275

chromate transport protein - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: F75275

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.V.;

S.; Smith, H.O.; Venter, D.C.; Fraser, C.M.

Science 285; 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: F75275

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-400 <WHI>

A:Cross-references: UNIPROT:Q9R8S2; GB:AE002072; GB:AE000513; NID:G6460231; PDB:AA11955

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2413

A:Map position: 1

C:Superfamily: chromate resistance protein A

Query Match 1.3%; Score 7; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 GLVWLP 337
|||
Db 216 GLVWLP 222

RESULT 52

C83464
hypothetical protein PA1441 [imported] - Pseudomonas aeruginosa (strain PA01)
C:/Species: Pseudomonas aeruginosa
C:/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:/Accession: C83464
R/Stover, C.K.; Pham, X.Q.; Errin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.
adman, S.; Yuen, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lartig, K.; Lam,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:/Reference number: A82950; MUID:20437337; PMID:10984043
A:/Accession: C83464
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-427 <STO>
A:/Cross-references: UNIPROT:Q91306; GB:AE004574; GB:AE004091; NID:g9947391; PIDN:AAG0483
C:/Genetics:
A:/Gene: PA1441

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 427;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GDEPRLA 64
DB 399 GDEPRLA 405

RESULT 53
D70468
conserved hypothetical protein eq_1964 - Aquifex aeolicus
C:/Species: Aquifex aeolicus
C:/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:/Accession: D70468
R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O.
V.
Nature 392, 353-358, 1998
A:/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:/Reference number: A70300; MUID:9819666; PMID:9537320
A:/Accession: D70468
A:/Status: preliminary; nucleic acid sequence not shown; translation not shown
A:/Molecule type: DNA
A:/Residues: 1-429 <AO>
A:/Cross-references: UNIPROT:O67776; GB:AE000765; NID:g2984199; PIDN:AA07743.1; PID:g298
C:/Genetics:
A:/Gene: eq_1964
C:/Superfamily: Escherichia coli probable zinc proteinase yael

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 429;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 GQAAQSG 132
DB 346 GQAAQSG 352

RESULT 54
H84826
hypothetical protein At2g40230 [imported] - Arabidopsis thaliana
C:/Species: Arabidopsis thaliana (mouse-ear cress)
C:/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:/Accession: H84826
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bent, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euser, D.; Niemann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:/Reference number: A84420; MUID:20083487; PMID:10617197
A:/Accession: H84826
A:/Status: preliminary

A:/Molecule type: DNA
A:/Residues: 1-433 <STO>
A:/Cross-references: UNIPROT:Q9XEF2; GB:AE002093; NID:g6598942; PIDN:AA18737.1; GSPDB:GN
C:/Genetics:
A:/Gene: At2g40230
A:/Map position: 2

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 433;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 SVLSLSA 357
DB 22 SVLSLSA 28

RESULT 55
H87329
conserved hypothetical protein CC0651 [imported] - Caulobacter crescentus
C:/Species: Caulobacter crescentus
C:/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:/Accession: H87329
R/Niemann, W.C.; Feldlym, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.U.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:/Title: Complete genome sequence of Caulobacter crescentus.
A:/Reference number: A87249; MUID:21173698; PMID:11259647
A:/Accession: H87329
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-436 <STO>
A:/Cross-references: UNIPROT:Q9AFA0; GB:AE005673; NID:g13421866; PIDN:AAK2636.1; GSPDB:GN
C:/Genetics:
A:/Gene: CC0651

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 436;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 LRDFRDN 383
DB 253 LRDFRDN 259

RESULT 56
G96945
similar to ABC transporter (permease) CAC0374 [imported] - Clostridium acetobutylicum
C:/Species: Clostridium acetobutylicum
C:/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:/Accession: G96945
R/Nolling, U.; Breton, G.; Omelchenko, M.V.; Makarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:/Reference number: A96900; MUID:21359325; PMID:21359325
A:/Accession: G96945
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-438 <KOR>
A:/Cross-references: UNIPROT:Q97W26; GB:AE001437; PIDN:AAK78354.1; PID:G15023223; GSPDB:GN
C:/Genetics:
A:/Gene: CAC0374

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 438;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 IRSVRL 277
DB 344 IRSVRL 350

RESULT 57

567437

Damage and replication checkpoint control protein - fission yeast (Schizosaccharomyces fission)

N:Alternate names: WD repeat containing protein Ctr3

C:Species: Schizosaccharomyces pombe

C>Date: 20-Jul-1996 #sequence revision 13-Mar-1997 #text_change 16-Aug-2004

C/Accession: T37658; T43281; S67437

R:Comar, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

Submitted to the EMBL Data Library, February 1996

A:Reference number: 221732

A:Accession: T37658

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-446 <CO2>

A/Cross-references: UNIPROT:Q10272; EMBL:Z69729; NID:G1204167; PIDN:CAA93596.1; PID:e223

A:Experimental source: strain 972h; cosmid C1367

R:Saka, Y.; Esashi, F.; Matsusaka, T.; Mochida, S.; Yanagida, M.

Genes Dev. 11, 3387-3400, 1997

A>Title: Damage and replication checkpoint control in fission yeast is ensured by intera

A/Reference number: 222390; MUID:98070339; PMID:9407031

A/Accession: T43281

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-446 <SAR>

A/Cross-references: EMBL:AB008572; PIDN:BA23358.1

C:Genetics:

A:Gene: SPAC1367.08c; ctr3+

A:Map position: 1

A:Insertion: 66/3; 403/3

C:Function:

A>Description: may be involved in G1/S progression

A>Note: essential for viability

C:Superfamily: WD repeat homology

F:292-325/Domain: WD repeat homology <WD1>

Query Match	1.3%;	Score 7;	DB 2;	Length 446;
Best Local Similarity	100.0%;	Pred. No. 1.2e+02;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0;

Oy	362	LFTASND	368
Db	133	LFTASND	139

RESULT 58

GMEBT

Indole-3-glycerol-phosphate synthase (EC 4.1.1.48) / phosphoribosylanthranilate isomerase

N:Contains: indole-3-glycerol-phosphate synthase (EC 4.1.1.48); phosphoribosylanthranilate

C/Species: Salmonella typhimurium

C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004

C/Accession: A01132

R:Horowitz, H.; Van Arsdell, J.; Platt, T.

J. Mol. Biol. 169, 775-797, 1983

A>Title: Nucleotide sequence of the trpD and trpC genes of Salmonella typhimurium.

A/Reference number: A92907; MUID:84036180; PMID:6355484

A/Accession: A01132

A:Molecule type: DNA

A:Residues: 1-452 <HOR>

A/Cross-references: UNIPROT:P00910; GB:M30286; NID:G154394; PIDN:AAA27237.1; PID:G154397

C:Genetics:

A:Gene: trpC-trpF

A:Map position: 34 min

C:Function: <PPAI>

A>Description: phosphoribosylanthranilate isomerase catalyzes conversion of N-5'-phospho

A:Pathway: tryptophan biosynthesis

A>Note: third step; catalyzed by the trpF homology domain

C:Function: <IGPS>

A>Description: indole-3-glycerol phosphate synthase catalyzes the ring closure to indol-

A:Pathway: tryptophan biosynthesis

A>Note: fourth step; catalyzed by the trpC homology domain

C:Superfamily: trpC-trpF bifunctional enzyme; trpC homology; trpF homology

C:Keywords: carbon-carbon lyase; carboxy-lyase; intramolecular oxidoreductase; isomerase

F:4-252/Domain: trpC homology <TRC>
F:258-449/Domain: trpF homology <TRF>

Query Match	1.3%;	Score 7;	DB 1;	Length 452;
Best Local Similarity	100.0%;	Pred. No. 1.2e+02;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0;

Oy	352	VLSLSAV	358
Db	325	VLSLSAV	331

RESULT 59

AD0653

Indole-3-glycerol phosphate synthase [imported] - Salmonella enterica subsp. enterica ser

C/Species: Salmonella enterica subsp. enterica serovar Typh

A>Note: this species has also been called Salmonella typh

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C/Accession: AD0653

R:Farhail, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,

th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: AD0653

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-452 <PAR>

A/Cross-references: GB:AL513382; PIDN:CAD08407.1; PID:G16502450; GSPDB:GN00176

C:Genetics:

A:Gene: STY1326

C:Superfamily: trpC-trpF bifunctional enzyme; trpC homology; trpF homology

Query Match	1.3%;	Score 7;	DB 2;	Length 452;
Best Local Similarity	100.0%;	Pred. No. 1.2e+02;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0;

Oy	352	VLSLSAV	358
Db	325	VLSLSAV	331

RESULT 60

S50725

Hypothetical protein YNL206c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein NL346

C/Species: Saccharomyces cerevisiae

C>Date: 23-Aug-1995 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004

C/Accession: S50725; S63163; S49863

R:Donnaux, U.L.; Coster, F.; Purnelle, B.; Goffeau, A.

Yeast 10, 1639-1645, 1994

A>Title: A 21.7 kb DNA segment on the left arm of yeast chromosome XIV carries WH13, GCR2

A/Reference number: S50712; MUID:95242839; PMID:7725799

A/Accession: S50725

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-455 <DON>

A/Cross-references: UNIPROT:P40161; EMBL:X78698; NID:G600045; PIDN:CA55502.1; PID:G600050

R:Coster, F.; Donnaux, U.L.; Goffeau, A.; Purnelle, B.; Van Dyck, L.

submitted to the Protein Sequence Database, April 1996

A/Reference number: S63151

A/Accession: S63163

A:Molecule type: DNA

A:Residues: 1-455 <COS>

A/Cross-references: EMBL:Z71482; NID:G1302206; PID:G239612; PID:G1302207; MIPS:YNL206C

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:RTT106

A/Cross-references: SGD:S0005150

A:Map position: 14L

Query Match 1.3%; Score 7; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 QNFEAES 150
 |||||
 DB 358 QNFEAES 364

RESULT 61

hypothetical protein CPJ1070 [imported] - Chlamydomophila pneumoniae (strain J138)
 C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: C86624
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871562
 A:Accession: C86624
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-456 <STO>
 A:Cross-references: UNIPROT:Q92619; GB:BA000008; NID:98979443; PIDN:BA99277.1; GSPDB:GN
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: CPJ1070

Query Match 1.3%; Score 7; DB 2; Length 456;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 LQKLSRL 307
 |||||
 DB 288 LQKLSRL 294

RESULT 62

hypothetical protein CP0780 [imported] - Chlamydomophila pneumoniae (strains CWL029 and AR
 C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: H72000; A81538
 R:Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
 Nature Genet. 21, 385-389, 1999
 A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: H72000
 A:Molecule type: DNA
 A:Residues: 1-456 <ARN>
 A:Cross-references: UNIPROT:Q92619; GB:AE001687; GB:AE001363; NID:94377398; PIDN:AA01920
 A:Experimental source: strain CWL029
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis Mdpn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: A81538
 A:Molecule type: DNA
 A:Residues: 1-456 <REA>
 A:Cross-references: GB:AE002236; GB:AE002161; NID:97189693; PIDN:AAF38579.1; PID:9718969
 C:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: CPJ1070; CP0780

Query Match 1.3%; Score 7; DB 2; Length 456;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 LQKLSRL 307
 |||||
 DB 288 LQKLSRL 294

RESULT 63

hypothetical protein At2g31130 [imported] - Arabidopsis thaliana
 H64716
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: H64716
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Varkken, S.E.; Unayam, L.; Tallon, L.;
 Neus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A64420; MUID:20083487; PMID:10617197
 A:Accession: H64716
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-457 <STO>
 A:Cross-references: UNIPROT:O82271; GB:AE002093; NID:93746063; PIDN:AA063838.1; GSPDB:GN
 A:Genetics:
 A:Gene: At2g31130
 A:Map position: 2

Query Match 1.3%; Score 7; DB 2; Length 457;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 QPSLATS 109
 |||||
 DB 290 QPSLATS 296

RESULT 64

trab protein homolog - Spingomonas aromaticivorans plasmid pNL1
 T31237
 C:Species: Spingomonas aromaticivorans
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T31237
 R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; Ge
 Submitted to the EMBL Data Library, July 1998
 A:Description: Complete sequence of a 184 kb catabolic plasmid from Spingomonas aromatic
 A:Reference number: Z20992
 A:Accession: T31237
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-458 <ROM>
 A:Cross-references: UNIPROT:O85945; EMBL:AF079317; NID:93378261; PID:93378378; PIDN:AA00:
 C:Genetics:
 A:Genome: plasmid pNL1
 A:Note: trab

Query Match 1.3%; Score 7; DB 2; Length 458;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 125 QGQAQNS 131
 |||||
 DB 130 QGQAQNS 136

RESULT 65

AB0423
 probable outer membrane efflux lipoprotein lbeB [imported] - Yersinia pestis (strain CO92
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AB0423
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 illo, M.; Partridge, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dogan, G.;
 illo, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, T.
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AB0423
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-468 <XIR>
 A:Cross-references: UNIPROT:Q82BD5; GB:AL590842; P1DN:CAC92710.1; P1D:G15981405; GSPDB:C
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S43294
 R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
 A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
 A:Reference number: S43294; MUID:94195427; PMID:8145850
 A:Accession: S43294
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-495 <STO>
 A:Cross-references: UNIPROT:P43027; GB:U08337; NID:G488461; P1DN:AAA18778.1; P1D:G488462
 C:Superfamily: Inhibin

Query Match 1.3%; Score 7; DB 2; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 ETLVOSA 190
 |||||
 Db 221 ETLVOSA 227

RESULT 66
 S43294
 bone morphogenetic protein-related protein (GDF5) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S43294
 R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
 A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
 A:Reference number: S43294; MUID:94195427; PMID:8145850
 A:Accession: S43294
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-495 <STO>
 A:Cross-references: UNIPROT:P43027; GB:U08337; NID:G488461; P1DN:AAA18778.1; P1D:G488462
 C:Superfamily: Inhibin

Query Match 1.3%; Score 7; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
 |||||
 Db 271 LLDVRSV 277

RESULT 67
 C85789
 hypothetical protein 'yea' [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: C85789
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 528-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: C85789
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-496 <STO>
 A:Cross-references: UNIPROT:Q8XDT6; GB:AE005174; NID:G12515823; P1DN:AA656775.1; GSPDB:C
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: 'yea'
 C:Superfamily: hypothetical protein b1786

Query Match 1.3%; Score 7; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 PLLWRFL 375
 |||||
 Db 255 PLLWRFL 261

RESULT 68

JC2347
 growth/differentiation factor 5 - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: JC2347
 R:Hoetien, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.
 Biochem. Biophys. Res. Commun. 204, 646-652, 1994
 A:Title: Cloning and expression of recombinant human growth/differentiation factor 5.
 A:Reference number: JC2347; MUID:95071375; PMID:7980526
 A:Accession: JC2347
 A:Molecule type: DNA
 A:Residues: 1-501 <HOE>
 A:Cross-references: UNIPROT:P43026; GB:X80915; NID:G671524; P1DN:CAA56874.1; P1D:G671525
 C:Genetics:
 A:Gene: GDB:BMP9
 A:Cross-references: GDB:433948
 A:Introns: 211/1
 C:Superfamily: Inhibin
 C:Keywords: glycoprotein
 F:189/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:381/382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match 1.3%; Score 7; DB 2; Length 501;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
 |||||
 Db 277 LLDVRSV 283

RESULT 69
 A55452
 cartilage-derived morphogenetic protein 1 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
 C:Accession: A55452
 R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak,
 J. Biol. Chem. 269, 28227-28234, 1994
 A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth
 A:Reference number: A55452; MUID:95050604; PMID:7961761
 A:Accession: A55452
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-501 <CHA>
 A:Cross-references: UNIPROT:P43026; GB:U13660; NID:G600731; P1D:G600732
 C:Genetics:
 A:Gene: GDB:CDMP1
 A:Cross-references: GDB:438940
 C:Superfamily: Inhibin

Query Match 1.3%; Score 7; DB 2; Length 501;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
 |||||
 Db 277 LLDVRSV 283

RESULT 70
 T20121
 hypothetical protein F1A3.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T20121; T20742
 R:McMurray, A.
 submitted to the EMBL Data Library, April 1996
 A:Reference number: Z19225
 A:Accession: T20121
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-529 <WIL>

A/Cross-references: UNIPROT:Q18746; EMBL:Z70750; PIDN:CAA94749.1; GSPDB:GN00023; CESP:FL1A3
 A/Experimental source: clone C50F4
 R/McMurray, A.
 Submitted to the EMBL Data Library, April 1996
 A/Accession: T20742
 A/Status: preliminary; translated from GB/EMBL/DDBT
 A/Molecule type: DNA
 A/Residues: 1-529 <M12>
 A/Cross-references: EMBL:Z70751; PIDN:CAA94752.1; GSPDB:GN00023; CESP:FL1A3.2
 A/Experimental source: clone FL1A3
 C/Genetics:
 A/Gene: CESP:FL1A3.2
 A/Map position: 5
 A/Intons: 18/3; 64/3; 87/1; 188/1; 260/3; 429/3; 478/3

Query Match 1.3%; Score 7; DB 2; Length 529;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VRLIKRT 11
 Db 310 VRLIKRT 316

RESULT 71
 S74703
 hypothetical protein slr1301 - *Synechocystis* sp. (strain PCC 6803)
 C/Species: *Synechocystis* sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S74703
 R/Kaneho, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-116, 1996
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S74703
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-535 <KAN>
 A/Cross-references: UNIPROT:P72839; EMBL:D90901; GB:AB001339; NID:91651897; PIDN:BA1685
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C/Genetics:
 A/Start codon: GTG

Query Match 1.3%; Score 7; DB 2; Length 535;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 LQKLSRL 307
 Db 82 LQKLSRL 88

RESULT 72
 T49074
 hypothetical protein F4F15.60 - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C/Accession: T49074
 R/Alcazar, J.P.; Clabault, G.; Cotter, A.; Maché, R.; Mewes, H.W.; Rudd, S.; Lemcke, K.; submitted to the Protein Sequence Database, April 2000
 A/Reference number: Z25015
 A/Accession: T49074
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-540 <ALC>
 A/Cross-references: UNIPROT:Q9SV09; EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.60
 A/Experimental source: cultivar Columbia; BAC clone F4F15
 C/Genetics:
 A/Gene: ATSP:F4F15.60

A/Map position: 3
 A/Intons: 225/2; 280/2; 342/2; 365/1; 461/2; 521/2

Query Match 1.3%; Score 7; DB 2; Length 540;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 495 LPRGCGP 501
 Db 528 LPRGCGP 534

RESULT 73
 C86264
 protein F3F19.5 [imported] - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: C86264
 R/Rheologis, A.; Becker, J.R.; Palm, C.J.; Federpsiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; aneu, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.D.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ke, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: C86264
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-547 <STO>
 A/Cross-references: UNIPROT:Q9SAD8; GB:AB005172; NID:94850386; PIDN:AAD1056.1; GSPDB:GN000000000
 C/Genetics:
 A/Gene: F3F19.5
 A/Map position: 1

Query Match 1.3%; Score 7; DB 2; Length 547;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 346 LIDVRSV 352
 Db 440 LIDVRSV 446

RESULT 74
 B64939
 hypothetical protein b1786 - *Escherichia coli* (strain K-12)
 C/Species: *Escherichia coli*
 C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 C/Accession: B64939
 R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mau, B.; Saeo, Y.
 Science 277, 1453-1462, 1997
 A/Title: The complete genome sequence of *Escherichia coli* K-12.
 A/Reference number: A64720; MUID:97426617; PMID:9278503
 A/Accession: B64939
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-556 <BLAT>
 A/Cross-references: GB:AB000273; GB:U00096; NID:91788078; PIDN:AACT4856.1; PID:91788086;
 A/Experimental source: strain K-12, substrain MG1655
 C/Superfamily: hypothetical protein b1786

Query Match 1.3%; Score 7; DB 2; Length 556;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 369 PLIMRFL 375
 Db 315 PLIMRFL 321

RESULT 75

G90940
hypothetical protein Ecs2495 [imported] - Escherichia coli (strain O157:H7, substrain R)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: G90940
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Sasawara, N.; Yasunaga, T.; Kuhtara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A96229; MUID:21156231; PMID:11258796
A:Accession: G90940
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-556 <HAY>
A:Cross-references: UNIPROT:Q8XDT6; GB:BA000007; PIDN:BA835918.1; PID:913361962; GSEPD:G
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: Ecs2495
C:Superfamily: hypothetical protein b1786

Query Match 1.3%; Score 7; DB 2; Length 556;
Best local similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Caps 0;

CY 369 PLWRF 375
DB 315 PLWRF 321

Search completed: November 16, 2004, 07:32:28
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:21:20 ; Search time 195 Seconds

(without alignments)
1540.234 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 522
Sequence: 1 MRURVRLKRTWPLEVFETE.....DRFPPRPSRGRTDGRLSFM 522Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	490	93.9	522	1 FBX7_HUMAN	Q9Y311 homo sapien
2	490	93.9	522	2 CAG30377	Cag30377 homo sapi
3	31	5.9	361	2 O6Y017	O6Y017 gallus gall
4	31	5.9	361	2 AAP83452	AAP83452 gallus ga
5	26	5.0	523	2 O8K0A5	O8K0A5 mus musculu
6	11	2.1	478	2 Q6D859	Q6D859 xenopus lae
7	10	1.9	1265	2 Q86HP8	Q86HP8 dictyostell
8	8	1.5	185	2 Q8M2Z3	Q8M2Z3 helicoverpa
9	8	1.5	200	2 Q6U7Y3	Q6U7Y3 crinipellis
10	8	1.5	200	2 AAC74304	AAC74304 crinipell
11	8	1.5	300	2 Q6BK56	Q6BK56 debaryomyce
12	8	1.5	331	2 Q76BP2	Q76BP2 lepisosteus
13	8	1.5	331	2 BAD17904	BAD17904 lepisoste
14	8	1.5	353	2 Q62197	Q62197 caenorhabdi
15	8	1.5	355	2 Q6NA16	Q6NA16 rhodopseudo
16	8	1.5	355	2 CAE26813	CAE26813 rhodopseu
17	8	1.5	402	1 VEB2_HPV65	VEB2 HPV65
18	8	1.5	404	2 Q702V2	Q702V2 yersinia en
19	8	1.5	404	2 CAF25097	CAF25097 yersinia
20	8	1.5	628	2 Q9U1J3	Q9U1J3 mus musculu
21	8	1.5	686	2 Q98F09	Q98F09 rhizobium l
22	8	1.5	730	2 Q9SKK7	Q9SKK7 arabidopsis
23	8	1.5	758	2 Q7Q4C4	Q7Q4C4 anopheles g
24	8	1.5	1047	2 Q74BP1	Q74BP1 geobacter s
25	8	1.5	1047	2 AAR35321	AAR35321 geobacter
26	8	1.3	67	2 Q8TJ06	Q8TJ06 methanocarc
27	7	1.3	67	2 Q8SNT0	Q8SNT0 hapalemur g
28	7	1.3	80	2 Q7R6Q1	Q7R6Q1 giardia lam
29	7	1.3	80	2 Q76H60	Q76H60 salmonella
30	7	1.3	80	2 BAD15208	BAD15208 salmonell
31	7	1.3	82	2 Q7P7A6	Q7P7A6 fusobacteri

32	7	1.3	84	2 P74781	P74781 synecocyst
33	7	1.3	89	2 Q9G218	Q9G218 eretmoceru
34	7	1.3	89	2 Q9G966	Q9G966 eretmoceru
35	7	1.3	91	2 Q6GV22	Q6GV22 bos taurus
36	7	1.3	91	2 Q9ZV53	Q9ZV53 arabidopsis
37	7	1.3	91	2 Q89TW2	Q89TW2 bradyrhizob
38	7	1.3	92	2 Q7YMB6	Q7YMB6 oryza sativ
39	7	1.3	92	2 BAD17403	BAD17403 oryza sat
40	7	1.3	92	2 BAD17570	BAD17570 oryza sat
41	7	1.3	96	2 Q9Y0B7	Q9Y0B7 pyrococcus
42	7	1.3	105	2 Q81E48	Q81E48 bacillus ce
43	7	1.3	110	2 Q54878	Q54878 streptococc
44	7	1.3	111	2 Q8MT79	Q8MT79 drosophila
45	7	1.3	112	2 Q9ANA6	Q9ANA6 bradyrhizob
46	7	1.3	118	2 Q8HAE8	Q8HAE8 bacteriopho
47	7	1.3	120	2 Q8CLJ3	Q8CLJ3 yersinia pe
48	7	1.3	123	2 Q8CIU9	Q8CIU9 mus musculu
49	7	1.3	125	2 Q81RB0	Q81RB0 bacillus an
50	7	1.3	125	2 AAT31258	AAT31258 bacillus
51	7	1.3	131	1 SSB2_STRF3	SSB2_STRF3
52	7	1.3	131	1 SSB2_STRF5	SSB2_STRF5
53	7	1.3	140	2 Q8ZE27	Q8ZE27 yersinia pe
54	7	1.3	140	2 AAB62066	AAB62066 yersinia
55	7	1.3	141	2 Q973V4	Q973V4 sulfolobus
56	7	1.3	141	2 Q8C938	Q8C938 mus musculu
57	7	1.3	144	2 Q6XIE4	Q6XIE4 drosophila
58	7	1.3	144	2 Q8ABR0	Q8ABR0 bacteroides
59	7	1.3	144	2 AAR09909	AAR09909 drosophil
60	7	1.3	148	2 Q8GDK1	Q8GDK1 photorhabdu
61	7	1.3	149	2 Q94173	Q94173 oryza sativ
62	7	1.3	150	1 YAB7_MYCPN	YAB7_MYCPN
63	7	1.3	151	2 Q93VE4	Q93VE4 oryza sativ
64	7	1.3	152	2 Q7X9T7	Q7X9T7 geum rivale
65	7	1.3	160	1 PHAA_ANACY	PHAA_ANACY
66	7	1.3	160	1 PHAA_FREDI	PHAA_FREDI
67	7	1.3	160	1 PHAA_PORFE	PHAA_PORFE
68	7	1.3	160	2 Q8DU53	Q8DU53 streptococc
69	7	1.3	163	2 Q6MM00	Q6MM00 homo sapien
70	7	1.3	166	2 Q7OIG5	Q7OIG5 anopheles g
71	7	1.3	166	2 Q8G4L5	Q8G4L5 bifidobacte
72	7	1.3	167	2 Q9TH82	Q9TH82 clostridium
73	7	1.3	170	2 Q7V177	Q7V177 prochloroco
74	7	1.3	172	2 Q8T018	Q8T018 drosophila
75	7	1.3	182	2 Q7XJ34	Q7XJ34 brassica ra
76	7	1.3	182	2 Q8TVY3	Q8TVY3 pseudomonas
77	7	1.3	182	2 Q7TNH9	Q7TNH9 caenorhabdi
78	7	1.3	184	2 Q71H45	Q71H45 andrena acc
79	7	1.3	184	2 Q92BK4	Q92BK4 listeria in
80	7	1.3	184	2 AAQ07600	AAQ07600 andrena a
81	7	1.3	185	2 Q8NZV7	Q8NZV7 spodoptera
82	7	1.3	185	2 Q8WZW3	Q8WZW3 spodoptera
83	7	1.3	187	2 Q6KAW0	Q6KAW0 oryza sativ
84	7	1.3	187	2 Q8ET53	Q8ET53 oceanobacil
85	7	1.3	188	2 Q9YX11	Q9YX11 caenorhabdi
86	7	1.3	188	2 Q71GN9	Q71GN9 andrena vic
87	7	1.3	188	2 Q71GPI	Q71GPI andrena nyl
88	7	1.3	188	2 Q71GPI	Q71GPI andrena dol
89	7	1.3	188	2 Q71GZ1	Q71GZ1 andrena lem
90	7	1.3	188	2 Q71GZ2	Q71GZ2 andrena lev
91	7	1.3	188	2 Q71H03	Q71H03 andrena hum
92	7	1.3	188	2 Q71H51	Q71H51 andrena acc
93	7	1.3	188	2 Q6HPK4	Q6HPK4 bacillus th
94	7	1.3	188	2 Q73F15	Q73F15 bacillus ce
95	7	1.3	188	2 Q811Z9	Q811Z9 bacillus ce
96	7	1.3	188	2 Q81VW9	Q81VW9 bacillus an
97	7	1.3	188	2 AAS39128	AAS39128 bacillus
98	7	1.3	188	2 AAQ07598	AAQ07598 andrena a
99	7	1.3	188	2 AAQ07646	AAQ07646 andrena h
100	7	1.3	188	2 AAQ07656	AAQ07656 andrena l

ALIGNMENTS

RESULT 1
FBX7 HUMAN STANDARD; PRT; 522 AA.
AC O95YI1; O95H6; Q9UP21; O9UKT2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE F-box only protein 7.
GN Name=FBX07; Synonyms=FBX7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 41-522 FROM N.A.
RX MEDLINE=20003060; PubMed=10531035;
RA Cenciarelli C., Chatur D.S., Guardavaccaro D., Parks W., Vidal M.,
RA Pagano M.;
RL Curr. Biol. 9:1177-1179(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20399565; PubMed=10945468; DOI=10.1006/geno.2000.6211;
RA Ilyin G.P., Rialland M., Pigeon C., Guenou-Guillouzo C.;
RT "cDNA cloning and expression analysis of new members of the mammalian
RT F-box protein family";
RL Genomics 67:40-47(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clump M., Smink L.J., Atsough R., Almeida J.P., Abbate A.K.,
RA Baggley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.F., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burdill W.D., Burton V., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Evans K.D., Dockree C., Dodsworth S.J., Dublin R.M., Ellington A.G.,
RA Hammi P.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kersey J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leverisha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McEann O.T.,
RA McClell J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Seha H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soederlund C., Spragon L., Stewart C.A., Sulston J.E., Swann R.M.,
RA Vaadin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Mitoishi S., Kawasaki K., Sasaki T., Asakawa S., Kodoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.T.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Zhang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Brashaw H., Bourne S.,
RA Cordes M., Da Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Olesky P., Rottling T.,
RA Schreier P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA Kofl I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salter S.,
RA Budarf M.L., McDermid H.E., Johnson A.C., Wong A.C.C., Morrow B.E.,
RA Edlmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Perrard M., Kedra D., Serousi E., Franssen I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tiliun Y., Wright H.;
RT "The DNA sequence of human chromosome 22";

RL Nature 402:489-495(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Martina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadleron M., Soares M.B., Bonaldi M.F., Casavani T.J., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -1- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
CC (By similarity).
CC -1- SIMILARITY: Contains 1 F-box domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL, AF129537; AAF04471.1; -
DR EMBL, AF233225; AAF67155.1; -
DR EMBL, AL050254; CAB43356.1; -
DR EMBL, Z71183; CAB63143.1; -
DR EMBL, BC008361; AAH08361.1; -
DR Gene, HGNC:13586; FBX07.
DR MIM: 605648; -
DR GO: GO:0000151; C:ubiquitin ligase complex; TAS.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; TAS.
DR GO: GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR008945; SKP1_Skp2.
DR Pfam: PF00646; F-box; 1.
DR PROSITE: PS50181; FBX0; 1.
KW Ub1 conjugation pathway.
DR DOMAIN 329 375
FT CONFLICT 41 41 F-box.
FT CONFLICT 79 79 S->M (in Ref. 1).
FT CONFLICT 84 84 Q->H (in Ref. 1).
FT CONFLICT 115 115 M->P (in Ref. 1).
FT CONFLICT 169 169 M->I (in Ref. 1 and 4).
FT CONFLICT 224 224 M->L (in Ref. 1).
FT CONFLICT 241 241 P->H (in Ref. 1).
FT CONFLICT 248 248 P->N (in Ref. 1).
FT CONFLICT 328 328 M->L (in Ref. 1).
FT CONFLICT 413 413 M->L (in Ref. 1).
FT CONFLICT 475 475 F->L (in Ref. 1).
SQ SEQUENCE 522 AA; 58502 MW; CAE5E70A0744287A CRC64;
Query Match 93.9%; Score 490; DB 1; Length 522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
33 SLICWGVSSNTRFTITNYKOPLTGDEETLASGIYSGDLICILQDDIAPNPISSTD 92

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Db      33 SLCTGWGSSNTRFTITLNYKDPDLPDDEETLASVYGVSGDLICLLQDDIPAPNIPSSTD 92
Qy      93 SEHSSTQNNQOPSLATSSNOTSMQDEQPSPOGQAAGSGVWMDSDMGPSONFEASTQ 152
Db      93 SEHSSTQNNQOPSLATSSNOTSMQDEQPSPOGQAAGSGVWMDSDMGPSONFEASTQ 152
Qy      153 DNAMAGEGTFYSEBPMLCSESVGEQVPSHLETLVQSADCSNDALIVLHILMLESGY 212
Db      153 DNAMAGEGTFYSEBPMLCSESVGEQVPSHLETLVQSADCSNDALIVLHILMLESGY 212
Qy      213 IPGTEAKALSMPEKWLKSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
Db      213 IPGTEAKALSMPEKWLKSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
Qy      273 SVKRLQLLPESFICKKELGENVANITYKDLQKLSRLEFDQVLYPLAFTRQALNLPVFGI 332
Db      273 SVKRLQLLPESFICKKELGENVANITYKDLQKLSRLEFDQVLYPLAFTRQALNLPVFGI 332
Qy      333 VVLPBELKRIFFRLDVRVSLSAVCRDLFTASNDPLMRFLYLDFPDNTVAVQDIDM 392
Db      333 VVLPBELKRIFFRLDVRVSLSAVCRDLFTASNDPLMRFLYLDFPDNTVAVQDIDM 392
Qy      393 KELYRKRIHQKESPKGRFVWMLPSSSTHTIPFYNPPLHPRFPSSRLPGIIGGEYDQRP 452
Db      393 KELYRKRIHQKESPKGRFVWMLPSSSTHTIPFYNPPLHPRFPSSRLPGIIGGEYDQRP 452
Qy      453 TLPPYGDPISSLIPGGETPSQFPPLRPDPVGPLPGNPPLPGSGGNDRPFRRSRG 512
Db      453 TLPPYGDPISSLIPGGETPSQFPPLRPDPVGPLPGNPPLPGSGGNDRPFRRSRG 512
Qy      513 RPTDGRLSFM 522
Db      513 RPTDGRLSFM 522

```

RESULT 2

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CAG30377
ID CAG30377 PRELIMINARY; PRT; 522 AA.
AC CAG30377;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DE 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE FBX07 protein.
GN FBX07
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Githam J.A.,
RA Cole C.G., Goward M.E., Aguado B., Malliya M., Mokrab Y., Huckle E.J.,
RA Beare D.M., Dunham I.;
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR456491; CAG30377.1; -
SQ SEQUENCE 522 AA; 58502 MW; CAEE570A0747287A CRC64;

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Query Match 93.9%; Score 490; DB 2; Length 522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      213 IPGTEAKALSMPEKWLKSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
Db      213 IPGTEAKALSMPEKWLKSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
Qy      273 SVKRLQLLPESFICKKELGENVANITYKDLQKLSRLEFDQVLYPLAFTRQALNLPVFGI 332
Db      273 SVKRLQLLPESFICKKELGENVANITYKDLQKLSRLEFDQVLYPLAFTRQALNLPVFGI 332
Qy      333 VVLPBELKRIFFRLDVRVSLSAVCRDLFTASNDPLMRFLYLDFPDNTVAVQDIDM 392
Db      333 VVLPBELKRIFFRLDVRVSLSAVCRDLFTASNDPLMRFLYLDFPDNTVAVQDIDM 392
Qy      393 KELYRKRIHQKESPKGRFVWMLPSSSTHTIPFYNPPLHPRFPSSRLPGIIGGEYDQRP 452
Db      393 KELYRKRIHQKESPKGRFVWMLPSSSTHTIPFYNPPLHPRFPSSRLPGIIGGEYDQRP 452
Qy      453 TLPPYGDPISSLIPGGETPSQFPPLRPDPVGPLPGNPPLPGSGGNDRPFRRSRG 512
Db      453 TLPPYGDPISSLIPGGETPSQFPPLRPDPVGPLPGNPPLPGSGGNDRPFRRSRG 512
Qy      513 RPTDGRLSFM 522
Db      513 RPTDGRLSFM 522

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RESULT 3

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Q6Y0L7
ID Q6Y0L7 PRELIMINARY; PRT; 361 AA.
AC Q6Y0L7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE F-box only protein 7 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Emara M.G., Kim H.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY194289; AAP83452.1; -
DR EMBL; AY194289; AAP83452.1; JOINED.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS50181; FBOX; 1.
FT NON TER
SQ SEQUENCE 361 AA; 40110 MW; 51C54C0282833884 CRC64;

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Query Match 5.9%; Score 31; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 2,6e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      321 ROALNLPVPGVAVLPLELKRIFFRLDVR 351
Db      169 ROALNLPVPGVAVLPLELKRIFFRLDVR 199

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RESULT 4

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AAP83452
ID AAP83452 PRELIMINARY; PRT; 361 AA.
AC AAP83452;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE F-box only protein 7 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

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RN [1]
RP SEQUENCE FROM N.A.
RA Emera M.G., Kim H.;
RT "Genomic region of F-box only protein 7 in chicken.";
RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY194288; AAP83452.1; JOINED.
FT NON TER
SQ SEQUENCE 361 AA; 40110 MW; 51C54C0292833884 CRC64;

Query Match 5.9%; Score 31; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 2.6e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 321 RQALNPDVFGVLVPLELKIRIFRLDVS 351
    |||||
Db 169 RQALNPDVFGVLVPLELKIRIFRLDVS 199

RESULT 5
08KOAS PRELIMINARY; PRT; 523 AA.
AC 08KOAS;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F-box only protein 7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RC MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Warr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC STRAIN=FVB/N; TISSUE=Liver;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032153; AAH32153.1; -.
DR MGI; MGI:1917004; Fbxo7.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 523 AA; 57634 MW; ABFD250070C1FB5 CRC64;

Query Match 5.0%; Score 26; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 7.2e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 324 LNLDPVFGVLVPLELKIRIFRLDVS 349

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Db 325 LNLDPVFGVLVPLELKIRIFRLDVS 350
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RESULT 6
06DB59 PRELIMINARY; PRT; 478 AA.
AC 06DB59;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RC MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RC PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Warr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Embryo;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077283; AAH77283.1; -.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 53251 MW; 8C12F01E32C1873F CRC64;

Query Match 2.1%; Score 11; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 338 ELKIRIFRLD 348
    |||||
Db 320 ELKIRIFRLD 330

RESULT 7
086HP8 PRELIMINARY; PRT; 1265 AA.
ID 086HP8;
AC 086HP8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)

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DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910;
 RA Gloeckner G., Eichinger L., Szatranski K., Pachebat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 RA Tussagel B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.",
 RL Nature 418:79-85(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Baumgart C.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC116957; AA052522.1; -;
 DR InterPro: IPR002114; HPR_Ser_P_S.
 DR InterPro: IPR008940; Prenyl_Trans.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 1265 AA; 144025 MW; B925B84755265B1C CRC64;

Query Match 1.9%; Score 10; DB 2; Length 1265;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 349 VRSVLSLSAV 358
 |||||
 Db 165 VRSVLSLSAV 174

RESULT 8
 Q8M2Z3 PRELIMINARY; PRT; 185 AA.
 ID Q8M2Z3
 AC Q8M2Z3;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Acyl-CoA desaturase HassKSVE (Fragment).
 OS Helicoverpa assulta (Oriental tobacco budworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Noctuidae; Heliothinae; Helicoverpa.
 OX NCBI_TaxID=52344;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22412134; PubMed=12524345;
 RA Knipfle D.C., Rosenfield C.L., Nielsen R., You K.M., Jeong S.E.,
 RT "Evolution of the integral membrane desaturase gene family in moths
 and flies.",
 RL Genetics 162:1737-1752(2002).

DR EMBL: AF482807; AA028482.1; -;
 DR GO: GO:0005783; C:Endoplasmic reticulum; IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005506; F:Iron ion binding; IEA.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:000468; F:stearoyl-CoA 9-desaturase activity; IEA.
 DR InterPro: IPR001522; Desaturase.
 DR InterPro: IPR005804; Pa_desat.
 DR Pfam: PF00487; PA_desaturase; 1.
 DR PRINTS: PR00075; FACDSACRASE.
 FT NON_TER 1
 FT 185
 SQ SEQUENCE 185 AA; 21597 MW; 54B7BA00FA36FF7 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 30;

Matches 8; Conservative 0; Mismatches 0; Indels 0;
 Qy 44 TRFTITLN 51
 |||||
 Db 136 TRFTITLN 143

RESULT 9
 ID Q6U7Y3 PRELIMINARY; PRT; 200 AA.
 AC Q6U7Y3
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Hypothetical protein hyp14.
 GN Name=hyp14;
 OS Crinipellis perniciosa.
 OG Crinipellidae perniciosa.
 OC Mitochondrion.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Tricholomataceae; Crinipellis.
 OX NCBI_TaxID=153609;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Forinighieri E.F., Sardinha-Pinto N., Cotomacci C., Araujo M.R.R.,
 RA Digiamplieri L.A., Carazzone M.F., Cursi D.E., Bertolin R.B.,
 RA Castro L.A.B., Gramacho K., Goes-Neto A., Goncalves M.S.,
 RA Barbosa L.V., Fernandez L.G., Cascado J.C.M., Pereira G.A.G.,
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY376688; AA074304.1; -;
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Hypothetical protein; Mitochondrion.
 SQ SEQUENCE 200 AA; 22038 MW; F7A99538A8A64D36 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 349 VRSVLSLS 356
 |||||
 Db 87 VRSVLSLS 94

RESULT 10
 AA074304 PRELIMINARY; PRT; 200 AA.
 ID AA074304
 AC AA074304;
 DT 03-MAR-2004 (TReMBLrel. 27, Created)
 DT 03-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 03-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE Hypothetical protein hyp14.
 GN hyp14.
 OS Crinipellis perniciosa.
 OG Crinipellidae perniciosa.
 OC Mitochondrion.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Tricholomataceae; Crinipellis.
 OX NCBI_TaxID=153609;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Forinighieri E.F., Sardinha-Pinto N., Cotomacci C., Araujo M.R.R.,
 RA Digiamplieri L.A., Carazzone M.F., Cursi D.E., Bertolin R.B.,
 RA Castro L.A.B., Gramacho K., Goes-Neto A., Goncalves M.S.,
 RA Barbosa L.V., Fernandez L.G., Cascado J.C.M., Pereira G.A.G.,
 RT "The complete mitochondrial genome of Crinipellis perniciosa, the
 RT causal agent of witches' broom disease of cocoa.",
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY376688; AA074304.1; -;
 KW Hypothetical protein; Mitochondrion.
 SQ SEQUENCE 200 AA; 22038 MW; F7A99538A8A64D36 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 VRSVLSTS 356
 Db 87 VRSVLSTS 94

RESULT 11

ID 06BK56 PRELIMINARY; PRT; 300 AA.
 AC 06BK56;
 DT 01-OCT-2004 (TREMBLrel. 28, Created)
 DT 01-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Similar to CA2573|CASUZ Candida albicans CasUZ translation
 DE Initiation factor eIF2.
 GN ORFNames=DEHA0F262359;
 OS Debaryomyces hansenii (Yeast) (Torulasporea hansenii).
 OC Saccharomycetes; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
 OX NCBI_TaxID=4959;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RG GENOLITHUS;

RA Lafontaine I., de Montigny J., Marck C., Neveglisse C., Talla E.,
 RA Goffard N., Fraigneul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissiere A., Boyer J., Cattoilco L., Confantolieri F., de Barrovar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerret A., Kosul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikoleki M., Ozias S., Ozier-Kalogeropoulos C.,
 RA Pelenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Sennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zentou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissendach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in Yeasts";
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382138; CAG89828.1; -;
 KW Initiation factor.
 SQ SEQUENCE 300 AA; 33796 MW; 043AE9504267674B CRC64;

Query Match 1.5%; Score 8; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 SLETYOS 189
 Db 122 SLETYOS 129

RESULT 12
 ID 076BF2 PRELIMINARY; PRT; 331 AA.
 AC 076BF2;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Fructose-bisphosphate aldolase C (Fragment).
 OS Lepisosteus osseus (Long-nosed gar).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
 OC Lepisosteus.
 OX NCBI_TaxID=34771;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kikugawa K., Katoh K., Kuraku S., Sakurai H., Ishida O., Iwabe N.,

RA Miyata T.;
 RT "Basal jawed vertebrate phylogeny inferred from multiple nuclear DNA-
 RT coded genes";
 RL BMC Biol. 2:3-3(2004).
 DR EMBL; AB113390; BADI7904.1; -;
 DR InterPro; IPR000741; Aldolase_1.
 DR Pfam; PF00274; Glycolytic_1.
 DR Prodom; PP001128; Aldolase_1; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_1; 1.
 FT NON_TER
 SQ SEQUENCE 331 AA; 35835 MW; 26DB5C3FF4C3413A CRC64;

Query Match 1.5%; Score 8; DB 2; Length 331;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 ETLYOSAD 191
 Db 49 ETLYOSAD 56

RESULT 13
 ID BADI7904 PRELIMINARY; PRT; 331 AA.
 AC BADI7904;
 DT 01-JUN-2004 (TREMBLrel. 27, Created)
 DT 01-JUN-2004 (TREMBLrel. 27, Last sequence update)
 DT 01-JUN-2004 (TREMBLrel. 27, Last annotation update)
 DE Fructose-bisphosphate aldolase C (Fragment).
 OS Lepisosteus osseus (Long-nosed gar).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
 OC Lepisosteus.
 OX NCBI_TaxID=34771;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kikugawa K., Katoh K., Kuraku S., Sakurai H., Ishida O., Iwabe N.,
 RA Miyata T.;
 RT "Basal jawed vertebrate phylogeny inferred from multiple nuclear DNA-
 RT coded genes";
 RL BMC Biol. 2:3-3(2004).
 DR EMBL; AB113390; BADI7904.1; -;
 FT NON_TER
 SQ SEQUENCE 331 AA; 35835 MW; 26DB5C3FF4C3413A CRC64;

Query Match 1.5%; Score 8; DB 2; Length 331;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 ETLYOSAD 191
 Db 49 ETLYOSAD 56

RESULT 14
 ID 062197 PRELIMINARY; PRT; 353 AA.
 AC 062197;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein F32A11.3.
 GN Name=F32A11.3;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for

RT Investigating biology.";
 RL Science 282:2012-2018(1998).
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Smye R.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z81521; CAB04225.1; -.
 DR PIR; T21616; T21616.
 DR WormPep; F32A11.3; CE17739.
 KM Hypothetical protein.
 SQ SEQUENCE 353 AA; 38773 MW; 1435DF5F7C1F2416 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 353;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 350 RSVSLSA 357
 DB 53 RSVSLSA 60

RESULT 15
 O6NA16 PRELIMINARY; PRT; 355 AA.

DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Nitrogen-fixing NifU, C-terminal.
 GN OrderedLocusNames=RP1370;
 OS Rhodopseudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=1076;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodopseudomonas palustris.";
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; BX572597; CAE26813.1; -.
 DR InterPro; IPR01075; NifU_C.
 DR Pfam; PF01106; NifU; 1.
 DR ProDom; PD002830; NifU_C; 1.
 KM Complete proteome.
 SQ SEQUENCE 355 AA; 39283 MW; 7E37E937A2E431F0 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 353;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 355 LSAVCRDL 362
 DB 98 LSAVCRDL 105

RESULT 16
 CAE26813

ID CAE26813 PRELIMINARY; PRT; 355 AA.

AC CAE26813;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Nitrogen-fixing NifU, C-terminal.
 GN RPA1370.
 OS Rhodopseudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=1076;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodopseudomonas palustris.";
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; BX572597; CAE26813.1; -.
 SQ SEQUENCE 355 AA; 39283 MW; 7E37E937A2E431F0 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 353;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 355 LSAVCRDL 362
 DB 98 LSAVCRDL 105

RESULT 17
 VE2_HP065 STANDARD; PRT; 402 AA.

AC 007851;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Regulatory protein E2.
 GN Name=E2;
 OS Human papillomavirus type 65.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=28312;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93276568; PubMed=8389082;
 RA Egawa K., Delius H., Matsukura T., Kawashima M., de Villiers E.M.;
 RT "Two novel types of human papillomavirus, HPV 63 and HPV 65:
 RT comparisons of their clinical and histological features and DNA
 RT sequences to other HPV types.";
 RL Virology 194:789-799(1993).
 CC -1- FUNCTION: E2 regulates viral transcription and DNA replication. It
 CC binds to the E2R3 response element (5'-ACNNNNNGGT-3') present in
 CC multiple copies in the regulatory region. It can either activate
 CC or repress transcription depending on E2R3's position with regards
 CC to proximal promoter elements. Repression occurs by sterically
 CC hindering the assembly of the transcription initiation complex.
 CC The E1-E2 complex binds to the origin of DNA replication.
 CC -1- SUBUNIT: Binds DNA as a dimer.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; X70829; U0450174.1; -.
 DR HSSP; P06790; L14.
 DR InterPro; IPR000427; E2_N.
 DR InterPro; IPR001866; E2_C.
 DR InterPro; IPR009021; Viral_DNA_bd.
 DR Pfam; PF00511; PVP_E2_C; 1.
 DR Pfam; PF00508; PVP_E2_N; 1.
 DR ProDom; PD000672; E2_C; 1.
 DR ProDom; PD000678; E2_N; 1.

KW Activator; DNA replication; DNA-binding; Early protein;
 KW Nuclear protein; Repressor; Trans-acting factor;
 KW Transcription regulation;
 SQ SEQUENCE 402 AA; 45552 MW; C7BA2B5325919FP4 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 402;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 PGPGETPS 473
 DB 266 PGPGETPS 273

RESULT 18

ID Q702V2 PRELIMINARY; PRT; 404 AA.
 AC Q702V2;
 DT 05-JUL-2004 (TRMBLrel. 27, Created)
 DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE Putative outer membrane efflux protein.
 OS Yersinia enterocolitica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=630;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=6471/76;
 RA Skurnik M., Lahtinen P., Brzezinska A.;
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ626755; CAF25097.1; -
 DR InterPro; IPR006143; HlyD.
 DR InterPro; IPR003423; OEP.
 DR InterPro; IPR010131; RND_outer_NodT.
 DR Pfam; PF02321; OEP; 1
 DR TIGRFAMs; TIGR01730; RND_mfp; 1.
 DR TIGRFAMs; TIGR01845; RND_outer_NodT; 1.
 SQ SEQUENCE 404 AA; 42501 MW; C7CB6686BE6571F0 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 183 LETLYQSA 190
 DB 156 LETLYQSA 163

RESULT 19

CAF25097 PRELIMINARY; PRT; 404 AA.
 ID CAF25097;
 AC CAF25097;
 DT 02-MAR-2004 (TRMBLrel. 27, Created)
 DT 02-MAR-2004 (TRMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TRMBLrel. 27, Last annotation update)
 DE Putative outer membrane efflux protein.
 OS Yersinia enterocolitica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=630;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=6471/76;
 RA Skurnik M., Lahtinen P., Brzezinska A.;
 RL "Temperature and growth phase regulate the transcription of the O-antigen gene cluster of Yersinia enterocolitica O:3.",
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ626755; CAF25097.1; -
 KW Helicase.

SQ SEQUENCE 404 AA; 42501 MW; C7CB6686BE6571F0 CRC64;
 Query Match 1.5%; Score 8; DB 2; Length 404;

Best Local Similarity 100.0%; Pred. No. 61;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 183 LETLYQSA 190
 DB 156 LETLYQSA 163

RESULT 20

ID Q9U133 PRELIMINARY; PRT; 628 AA.
 AC Q9U133;
 DT 01-OCT-2000 (TRMBLrel. 15, Created)
 DT 01-OCT-2000 (TRMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE Netrin 4 (Beta netrin).
 GN Name=Netn4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR;
 RA MEDLINE=20400106; PubMed=10940631;
 RA Yin Y., Sanes J.R., Miner J.H.;
 RL "Identification and expression of mouse netrin-4.",
 RL Mech. Dev. 96:115-119(2000).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;
 RA MEDLINE=20493277; PubMed=11038171;
 RA Koch W., Muirrell J.B., Hunter D.D., Olson P.F., Jin W., Keene D.R.,
 RA Brunken W.J., Burgess R.E.;
 RL "A novel member of the netrin family, beta-netrin, shares homology with the beta chain of laminin. Identification, expression, and functional characterization.";
 RL J. Cell Biol. 151:221-234(2000).

DR EMBL; AF268066; AAF91404.1; -
 DR EMBL; AF281278; AAG30823.1; -
 DR HSSP; P02468; INPE.
 DR MGD; MGI:1888978; Ntn4.
 DR GO; GO:0016322; P:neuronal remodeling; IDA.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR008978; Gal_bind-like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR008211; Laminin_N.
 DR InterPro; IPR001134; Netrin_C.
 DR InterPro; IPR008993; TIMP-like.
 DR Pfam; PF00053; Laminin_EGF; 3.
 DR Pfam; PF00055; Laminin_N; 1.
 DR Pfam; PF01759; NTR; 1.
 DR PRINTS; PRO0011; EGF_LAMININ.
 DR SMART; SM00643; C345C; 1.
 DR SMART; SM00180; EGF_Lam; 3.
 DR SMART; SMO0136; LAMNT; 1.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
 DR PROSITE; PS50189; NTR; 1.
 KW Laminin EGF-like domain.
 SQ SEQUENCE 628 AA; 69896 MW; 474F74745F236C7 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 628;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 LVRRLKLR 10
 DB 224 LVRRLKLR 231

RESULT 21
 Q98FQ3

ID Q98FC9 PRELIMINARY; PRT; 686 AA.
AC Q98FC9;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE M13659 protein.
GN OrderedLocustNames=ml13659;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Pyliobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneke T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Kimura T.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.,
RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RT DNA Res. 7:331-338(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MAF303099;
RX MEDLINE=21082936; PubMed=11214974;
RA Kaneke T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Kimura T.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.,
RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti (supplement).";
RT DNA Res. 7:381-406(2000).
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL: AP003002; BAB50508.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO: GO:0007600; F:sensory perception; IEA.
DR GO: GO:0000160; P:two-component signal transduction system (p. . .); IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR011006; CheY_like.
DR InterPro: IPR003018; GAF_like.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR003661; His_kin_N.
DR InterPro: IPR009082; His_kin_homodm.
DR InterPro: IPR001005; Myb_DNA_binding.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000014; PAS.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF01590; GAF_1.
DR Pfam: PF02518; HATPase_C_1.
DR Pfam: PF00512; HSKA_1.
DR Pfam: PF00989; PAS_1.
DR Pfam: PF00072; Response_reg_1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR PRODOM: PD000039; Response_reg_1.
DR SMART: SM00065; GAF_1.
DR SMART: SM00387; HATPase_C_1.
DR SMART: SM00388; HSKA_1.
DR SMART: SM00086; PAC_1.
DR SMART: SM00091; PAS_1.
DR SMART: SM00448; REC_1.
DR TIGRFAMs: TIGR00229; sensory_box_1.
DR PROSITE: PS50109; HIS_KIN_1.
DR PROSITE: PS00037; MYB_1; UNKNOWN_1.

DR PROSITE: PS50112; PAS_1.
DR PROSITE: PS50110; RESPONSE_REGULATORY_1.
KW Complete proteome; kinase; phosphorylation; sensory transduction;
KW transferase.
SQ SEQUENCE 686 AA; 75044 MW; A50DD3932CC4FBE9 CRC64;
QY Query Match 1.5%; Score 8; DB 2; Length 686;
DB Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 347 LDVRSVLS 354
DB 669 LDVRSVLS 676
RESULT 22
ID Q9SKK7 PRELIMINARY; PRT; 730 AA.
AC Q9SKK7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein Atg25420.
GN Name=Atg25420;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Shee T.P., Fujii C.Y., Shen M., Vanaken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Rinning C.M., Benito M.-I.,
RA Carreira A.J., Creasy T.H., Buell C.R., Town C.D., Newman W.C.,
RA Frazer C.M., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 WD repeats.
DR EMBL: AC006300; AAD20702.2; -.
DR PIR: B84648; B84648.
DR InterPro: IPR006595; CTH_C.
DR InterPro: IPR006594; LISH_C.
DR InterPro: IPR001680; WD40.
DR InterPro: IPR011046; WD40_1like.
DR Pfam: PF00400; WD40_2.
DR SMART: SM00668; CTHLH_2.
DR SMART: SM00667; LISH_2.
DR SMART: SM00320; WD40_4.
DR PROSITE: PS50837; CTHLH_1.
DR PROSITE: PS50896; LISH_2.
DR PROSITE: PS50082; WD_REPEATS_2; 1.
DR PROSITE: PS50294; WD_REPEATS_REGION_1.
KW Hypothetical protein Repeat; WD repeat.
SQ SEQUENCE 730 AA; 82003 MW; 16205CE1D3769F88 CRC64;
QY Query Match 1.5%; Score 8; DB 2; Length 730;
DB Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 DILCILQ 79
DB 177 DILCILQ 184
RESULT 23
ID Q7Q4C4 PRELIMINARY; PRT; 758 AA.
AC Q7Q4C4;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)

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DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE AGCP11203 (Fragment).
GN Name=agCG48900; ORFNames=ENSNANGS00000015760;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 4 WD repeats.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008964; EAI2424.1; -.
DR InterPro; IPR006575; RMD.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40.4.
DR PRINTS; PR00320; GPROTEINRPT.
DR PROSITE; PS50908; RMD; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS50082; WD_REPEATS_2; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER 1
FT NON_TER 758
SQ SEQUENCE 758 AA; 84915 MW; D6F4CD3DBE5F0179 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 758;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 VLISAVC 359
DQ 202 VLISAVC 209

RESULT 24
Q74BT1 PRELIMINARY; PRT; 1047 AA.
ID Q74BT1
AC Q74BT1;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Fibronectin type III domain protein.
GN ORFNames=GSU1945;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
CX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RC PubMed=14671304; DOI=10.1126/science.1088727;
RA Heideberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Heideberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Kouri H.M., Feldblyum T.V., Uitterlind T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RA "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR35321.1; -.
DR TIGR; GSU1945; -.
DR InterPro; IPR002105; Dokerin_1.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000601; PKD.

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DR Pfam; PF00041; FN3; 1.
DR PROSITE; PS50853; FN3; 1.
SQ SEQUENCE 1047 AA; 106532 MW; 3C491EA2DAB493C0 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 ANDALIVL 202
DQ 987 ANDALIVL 994

RESULT 25
AAR35321 PRELIMINARY; PRT; 1047 AA.
ID AAR35321
AC AAR35321;
DT 02-MAR-2004 (TREMblrel. 27, Created)
DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMblrel. 27, Last annotation update)
DE Fibronectin type III domain protein.
GN GSU1945.
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
CX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RC PubMed=14671304;
RA Heideberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Heideberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Kouri H.M., Feldblyum T.V., Uitterlind T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RA "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969(2003).
DR EMBL; AE017214; AAR35321.1; -.
DR TIGR; GSU1945; -.
SQ SEQUENCE 1047 AA; 106532 MW; 3C491EA2DAB493C0 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 ANDALIVL 202
DQ 987 ANDALIVL 994

RESULT 26
Q8TU06 PRELIMINARY; PRT; 67 AA.
ID Q8TU06
AC Q8TU06;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Helix-turn-helix family protein.
GN OrderedLocustNames=MA3984;
OS Methanococcus acetiivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
CX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RC MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Deatellano K., Johnson R.,

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RA Linton L., McEwan P., McKernan K., Talamas J., Tittrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.W.,
 RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umayam L.A., White O., White R.H., de Maccario E.C.,
 RA Ferry J.G., Jarrell K.F., Jing H., Maccario A.J.L., Paulsen I.T.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Vander B.,
 RA Metcalf W.W., Birren B.,
 RT "The genome of *Methanoscobia acetiivorans* reveals extensive metabolic
 RT and physiological diversity.";
 RL Genome Res. 12:532-542 (2002).
 DR EMBL: AEO1110; F:DNA binding; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR InterPro: IPR001387; HTH_3.
 DR InterPro: IPR010982; Lambda_like_DNA.
 DR Pfam: PF01381; HTH_3; 1.
 DR SMART: SMO0530; HTH_XRE; 1.
 DR PROSITE: PS50943; HTH_CROCI; 1.
 KM Complete proteome.
 SQ SEQUENCE 67 AA; 7746 MW; C22489D51A0B9DD6 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 KLSRLFK 309
 DB 47 KLSRLFK 53

RESULT 27
 OGSNT0
 ID OGSNT0 PRELIMINARY; PRT; 67 AA.
 AC OGSNT0;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN Name:HagG-DRB;
 OS Haploleum griseus griseus.
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Haploleum.
 OX NCBI_TaxID=122219;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Go Y., Saita Y., Kawamoto Y., Rakotoarisoa G., Randrianjafo A.,
 RA Koyama N., Hirai H.,
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB078293; BAB8506.1;
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO: GO:0019884; P:antigen presentation, exogenous antigen; IEA.
 DR GO: GO:0019886; P:antigen processing, exogenous antigen via M. .; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR000353; MHC_II_beta.
 DR Pfam: PF00969; MHC_II_beta; 1.
 DR ProDom: PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 67 AA; 8128 MW; B0D7F590721E89F9 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RVRLIKR 10
 DB 2 RVRLIKR 8

RESULT 28
 Q7R6Q1

ID Q7R6Q1 PRELIMINARY; PRT; 80 AA.
 AC Q7R6Q1;
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE GLP 170.54038.54280.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Segin M.L.;
 RT "Direct sequence of the Giardia lamblia genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AACB01000001; EAA42946.1;
 DR InterPro: IPR002453; Beta_tubulin.
 DR PROSITE: PS00228; TUBULIN_E_AUTOREG; UNKNOWN 1.
 SQ SEQUENCE 80 AA; 9004 MW; C1CGB76CBA4CAB8E CRC64;

Query Match 1.3%; Score 7; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 SHRLSL 34
 DB 10 SHRLSL 16

RESULT 29
 O76H60
 ID O76H60 PRELIMINARY; PRT; 80 AA.
 AC O76H60;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE ORF46.
 GN Name=orf46;
 OS Salmonella typhimurium bacteriophage ST104.
 OC Viruses.
 OX NCBI_TaxID=221029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=15071057;
 RA Tanaka K., Nishimori K., Makino S., Nishimori T., Kanno T.,
 RA Ishihara R., Samehima T., Akiba M., Nakazawa M., Yokomizo Y.,
 RA Uchida I.;
 RT "Molecular characterization of a prophage of *Salmonella enterica*
 RT serotype Typhimurium DT104.";
 RL J. Clin. Microbiol. 42:1807-1812 (2004).
 DR EMBL: AB102868; BAD15208.1;
 SQ SEQUENCE 80 AA; 8565 MW; 4715BB951676D57 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 LFKDQIV 313
 DB 44 LFKDQIV 50

RESULT 30
 BAD15208
 ID BAD15208 PRELIMINARY; PRT; 80 AA.
 AC BAD15208;
 DT 14-APR-2004 (TReMBLrel. 27, Created)
 DT 14-APR-2004 (TReMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TReMBLrel. 27, Last annotation update)

DE ORF46.
 GN ORF46.
 OS Salmonella typhimurium bacteriophage ST104.
 OC Viruses.
 RX NCBI_TaxID=221029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanaka K., Nishimori K., Makino S., Nishimori T., Kanno T.,
 RA Ishihara R., Sameshima T., Akiba M., Nakazawa M., Yokomizo Y.,
 RA Uchida I.,
 RT "Molecular Characterization of a Prophage of Salmonella enterica
 RT Serotype Typhimurium DT104."
 RL J. Clin. Microbiol. 42:1807-1812(2004).
 DR EMBL: AB102868; BAD15208.1; -
 SQ SEQUENCE 80 AA; 8565 MW; 4715HB9516766D57 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 307 LFKDQLV 313
 Db 44 LFKDQLV 50

RESULT 31
 ID 07P7A6 PRELIMINARY; PRT; 62 AA.
 AC 07P7A6.
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=FVW1647;
 OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 CC Fusobacterium.
 CX NCBI_TaxID=209882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 49256;
 RA Karpman V., Ivanova N., Anderson I., Reznik G., Bhattacharya A.,
 RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
 RA Haseikorn R., Overbeek R., Kyrides N.,
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AABR0100019; EAA24690.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 62 AA; 8526 MW; 8ED40FPADB00D6B1 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 245 GSSATLT 251
 Db 24 GSSATLT 30

RESULT 32
 ID P74781 PRELIMINARY; PRT; 84 AA.
 AC P74781.
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Ssl1707 protein.
 GN OrderedLocustNames=ssl1707;
 OS Synechocystis sp. (strain PCC 6803).
 CC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 CX NCBI_TaxID=1148;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugita M., Saito T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nanno K., Okumura S.,
 RA Saito S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.,
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions."
 RL DNA Res. 3:109-136(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.,
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 64% to 92% of the genome."
 RL DNA Res. 2:153-166(1995).
 DR EMBL: D64006; BAA10859.1; -
 DR PIR: S76012; S76012.
 DR HSSP: C9X078; 1JDO.
 DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.
 DR InterPro: IPR001455; SIRA_like.
 KW Complete proteome.
 SQ SEQUENCE 84 AA; 9257 MW; DA02DA1FP39DB97 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 178 QVPHSLE 184
 Db 49 QVPHSLE 55

RESULT 33
 ID 09G218 PRELIMINARY; PRT; 89 AA.
 AC 09G218.
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Cytochrome oxidase II (Fragment).
 OS Eremococcus queenslandensis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelegrina;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
 OC Aphelinidae; Aphelininae; Eremocerus.
 CX NCBI_TaxID=131217;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA De Barro P.J., Driver F., Naumann I.D., Schmidt S., Clarke G.M.,
 RA Curran U.,
 RT "Descriptions of three species of Eremocerus Halteman (Hymenoptera:
 RT Aphelinidae) parasitising Bemisia tabaci (Gennadius) (Hemiptera:
 RT Aleyrodidae) and Trialeurodes vaporariorum (Westwood) (Hemiptera:
 RT Aleyrodidae) in Australia based on morphological and molecular data."
 RL Aust. J. Entomol. 39:259-269(2000).

-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
 chain that catalyzes the reduction of oxygen to water. Subunits 1-
 3 form the functional core of the enzyme complex. Subunit 2
 transfers the electrons from cytochrome c via its binuclear copper
 A center to the bimetallic center of the catalytic subunit 1 (By
 similarity).
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 c + 2 H(2)O.
 CC -!- COFACTOR: Copper A (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane (By similarity).

CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
 DR EMBL: AF275294; AAG25098.1; -
 DR EMBL: AF275287; AAG25091.1; -
 DR EMBL: AF275288; AAG25092.1; -
 DR EMBL: AF275289; AAG25093.1; -
 DR EMBL: AF275290; AAG25094.1; -
 DR EMBL: AF275291; AAG25095.1; -
 DR EMBL: AF275292; AAG25096.1; -
 DR EMBL: AF275293; AAG25097.1; -
 DR GO: 0016020; C:membrane; IEA.
 DR GO: 00055739; F:copper ion binding; IEA.
 DR GO: 0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO: 0004118; F:electron transport; IEA.
 DR InterPro: IPR001505; Copper_CuA.
 DR InterPro: IPR008972; Cupredoxin.
 DR Pfam: PF00116; COX2; 1.1; Cyt_c_ox_2.
 DR PRINTS: PR01166; CYCOXIDASEII.
 DR PRODOM: PD000131; Copper_CuA; 1.
 DR Copper; Electron transport; Inner membrane; Mitochondrion;
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10424 MW; 056B831A018474A2 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 343 IFRLLDV 349
 Db 26 IFRLLDV 32
 RESULT 34
 Q9G9G6 PRELIMINARY; PRT; 89 AA.
 AC Q9G9G6;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Cytochrome oxidase II (Fragment).
 OS Eremocerus queenslandensis.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
 OC Aphelinidae; Aphelininae; Eremocerus.
 OX NCBI_TaxID=111217;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA De Barro P.J., Driver F., Naumann I.D., Schmidt S., Clarke G.M.,
 RA Curran J.;
 RT "Descriptions of three species of Eremocerus Haldeman (Hymenoptera:
 RT Aphelinidae) parasitising Bemisia tabaci (Gennadius) (Hemiptera:
 RT Aleyrodidae) and Trialeurodes vaporariorum (Westwood) (Hemiptera:
 RT Aleyrodidae) in Australia based on morphological and molecular data.";
 RL Aust. J. Entomol. 39:259-269(2000).
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
 CC 3 form the functional core of the enzyme complex. Subunit 2
 CC transfers the electrons from cytochrome c via its binuclear copper
 CC A center to the binuclear center of the catalytic subunit 1 (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferriycyclochrome
 CC c + 2 H(2)O.
 CC -1- COFACTOR: Copper A (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
 DR EMBL: AF275295; AAG25099.1; -
 DR GO: 0016020; C:membrane; IEA.
 DR GO: 00055739; C:mitochondrion; IEA.

DR GO: 0005507; F:copper ion binding; IEA.
 DR GO: 0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO: 0006118; F:electron transport; IEA.
 DR InterPro: IPR001505; Copper_CuA.
 DR InterPro: IPR008972; Cupredoxin.
 DR InterPro: IPR002429; Cyt_c_ox_2.
 DR Pfam: PF00116; COX2; 1.1.
 DR PRINTS: PR01166; CYCOXIDASEII.
 DR PRODOM: PD000131; Copper_CuA; 1.
 DR Copper; Electron transport; Inner membrane; Mitochondrion;
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10442 MW; E12A831D6B29B3C8 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 343 IFRLLDV 349
 Db 26 IFRLLDV 32
 RESULT 35
 Q6GV22 PRELIMINARY; PRT; 91 AA.
 AC Q6GV22;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Myeloid differentiation factor 88 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Werling D.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A634627; AAT48485.1; -
 DR InterPro: IPR00157; TIR.
 DR PROSITE: PS50104; TIR; 1.
 FT NON_TER 1 1
 FT NON_TER 91 91
 SQ SEQUENCE 91 AA; 10658 MW; 37E1C22DB6DBE463 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 219 AKALSM 225
 Db 85 AKALSM 91
 RESULT 36
 Q9ZVS3 PRELIMINARY; PRT; 91 AA.
 AC Q9ZVS3;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE F15K9.18.
 GN Name=F15K9.18;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vysotskaya V.S., Schwartz J.R., Toriumi M., Yu G., Li J., Liu S.,

RA Kremenetskaia I., Luos J., Araujo R., Buehler E., Conway A.B.,
 RA Dever K., Feng J., Kim C., Li Y., Shinn P., Sun H., Davis R.W.,
 RA Scler J.R., Federspiel N.A., Theologis A.,
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC005278; AAC72126.1; -
 DR PIR: B6163; B6163.
 SQ SEQUENCE 91 AA; 10600 MW; EBCB45170E6D1CA4 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 316 LLAFTRO 322
 Db 80 LLAFTRO 86

RESULT 37
 Q89TW2 PRELIMINARY; PRT; 91 AA.
 ID Q89TW2
 AC Q89TW2
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Bs11884 protein.
 GN OrderedLocustNames=bs11884;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCB1_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Ideawa K., Iriyuchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.,
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL: AP005941; BAC67149.1; -
 DR InterPro: IPR009056; Cytochrome_C.
 KW Complete proteome.
 SQ SEQUENCE 91 AA; 9786 MW; B36FA66807EAA53 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 439 LPPGIIIG 445
 Db 67 LPPGIIIG 73

RESULT 38
 Q6YWB6 PRELIMINARY; PRT; 92 AA.
 ID Q6YWB6
 AC Q6YWB6
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 01-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Hypothetical protein P0501B09.15 (Hypothetical protein
 DE P0584E12.42).
 GN Name=P0501B09.15; Synonyms=P0584E12.42;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eubartoideae; Oryzaceae; Oryza.
 OX NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.,
 RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.,

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RL (2)
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.,
 RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP005787; BAD17570.1; -
 DR EMBL: AP005591; BAD17403.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 92 AA; 9772 MW; 085A4B6C65893581 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 509 PSRGRT 515
 Db 7 PSRGRT 13

RESULT 39
 BAD17403 PRELIMINARY; PRT; 92 AA.
 ID BAD17403
 AC BAD17403
 DT 10-MAY-2004 (TRENBLrel. 27, Created)
 DT 10-MAY-2004 (TRENBLrel. 27, Last sequence update)
 DT 10-MAY-2004 (TRENBLrel. 27, Last annotation update)
 DE Hypothetical protein P0584E12.42.
 GN P0584E12.42
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eubartoideae; Oryzaceae; Oryza; Oryza sativa.
 OX NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Katayose Y.,
 RT "Oryza sativa nipponbare (Ga3) genomic DNA, chromosome 9, PAC
 RT clone:P0584E12.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP005591; BAD17403.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 92 AA; 9772 MW; 085A4B6C65893581 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 509 PSRGRT 515
 Db 7 PSRGRT 13

RESULT 40
 BAD17570 PRELIMINARY; PRT; 92 AA.
 ID BAD17570
 AC BAD17570
 DT 10-MAY-2004 (TRENBLrel. 27, Created)
 DT 10-MAY-2004 (TRENBLrel. 27, Last sequence update)
 DT 10-MAY-2004 (TRENBLrel. 27, Last annotation update)
 DE Hypothetical protein P0501B09.15.
 GN P0501B09.15
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eubartoideae; Oryzaceae; Oryza; Oryza sativa.
 OX NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.,
 RA "Oryza sativa nipponbare (Ga3) genomic DNA, chromosome 9, PAC
 RT clone:P0501B09.";

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005787; BABI750.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 92 AA; 9772 MW; 085A4BBC65893581 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 92;
 Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 PSRGRPT 515
 Db 7 PSRGRPT 13

RESULT 41

QY00B7 PRELIMINARY; PRT; 96 AA.
 ID QY00B7
 AC QY00B7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=PYRAB09730; ORFNames=PAB7218;
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GES / Orsay;
 RX MEDLINE=22511545; PubMed=12622808;
 RA Cohen G.N., Barde V., Flament D., Galperin M., Hellis R., Lecomte O.,
 RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
 RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P;
 RT "An integrated analysis of the genome of the hyperthermophilic
 archaeon Pyrococcus abyssi."
 RL Mol. Microbiol. 47:1495-1512(2003).
 DR EMBL; AJ248285; CAB49787.1; -.
 DR PIR; B75134; B75134.
 DR InterPro; IPR002716; P1LT_N.
 DR Pfam; PF01850; PIN_1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 96 AA; 11308 MW; 88A44BBF5A352D6 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 96;
 Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 NDALIVL 202
 Db 63 NDALIVL 69

RESULT 42

Q81E48 PRELIMINARY; PRT; 105 AA.
 ID Q81E48
 AC Q81E48;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE 5-methylcytosine-specific restriction enzyme A (EC 3.1.21.-).
 GN OSFNames=BC1144;
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=226900;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RX Ivanova N., Sorokin A., Anderson I., Galleron N., Candillon B.,
 RA Kaparatel V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Cnu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.C.;

RT "Genome sequence of Bacillus cereus and comparative analysis with
 RT Bacillus anthracis."
 RL Nature 423:87-91(2003).
 DR EMBL; AE017004; AAP0911.1; -.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 KW Hydrolase.
 SQ SEQUENCE 105 AA; 11860 MW; 642040A37CFA113 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 105;
 Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 LFTASND 368
 Db 8 LFTASND 14

RESULT 43

Q54878 PRELIMINARY; PRT; 110 AA.
 ID Q54878
 AC Q54878;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SP1000; TRANSPOSON=Th5252;
 RX MEDLINE=94327488; PubMed=8051031;
 RA Kilic A.O., Vijayakumar M.N., al-Khalidi S.F.;
 RT "Identification and nucleotide sequence analysis of a transfer-related
 region in the streptococcal conjugative transposon Th5252."
 RL J. Bacteriol. 176:5145-5150(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SP1000; TRANSPOSON=Th5252;
 RA Vijayakumar M.N.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U29324; AAC98429.1; -.
 DR PIR; B55863; B55863.
 KW Hypothetical protein.
 SQ SEQUENCE 110 AA; 13053 MW; 3836A80B2F6D6B96 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 110;
 Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 YXDPLTG 58
 Db 21 YXDPLTG 27

RESULT 44

Q8MT79 PRELIMINARY; PRT; 111 AA.
 ID Q8MT79
 AC Q8MT79;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Ld08201p.
 GN Name=1(1)G0269;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;

Stapleton M., Brokstein P., Hong J., Agbayani A., Carlson J.,
 RA Campe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Munnell C.J., Nunco J., Pacleb J., Parasas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.,
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY118321; AAM48350.1; -
 DR Flybase: FBGN029067; 1(1)G0269.
 DR InterPro: IPR004274; NIF.
 DR Pfam: PF03031; NIF: 1.
 DR SMART: SM00577; CPDC: 1.
 DR SEQUENCE 111 AA; 12851 MW; B6B37648AA07E524 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 DRSVLS 354
 |||||
 DB 96 DRSVLS 102

RESULT 45

09ANA6 PRELIMINARY; PRT; 112 AA.
 AC 09ANA6;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE ID385.
 GN Name=Id385;
 OS Bradyrhizobium japonicum.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Bradyrhizobiaceae; Bradyrhizobium.
 OC NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1105PC4;
 RX MEDLINE=21101824; PubMed=1157954;
 RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
 RA Hennecke H.,
 RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
 RT DNA region of the Bradyrhizobium japonicum chromosome."
 RL J. Bacteriol. 183:1405-1412 (2001).
 DR EMBL: AF322012; AAG60867.1; -
 DR InterPro: IPR009056; Cytochrome C
 DR SEQUENCE 112 AA; 12069 MW; 98E2D9BF6ED5366 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 439 LPPGIG 445
 |||||
 DB 88 LPPGIG 94

RESULT 46

08HA8 PRELIMINARY; PRT; 118 AA.
 AC 08HA8;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Orf-118.
 GN Name=orf-118;
 OS Bacteriophage ST64T
 CC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
 OC NCB1_TaxID=173443;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22638307; PubMed=12754248;

Mwolawa P.T., Schmiegger H., Tucker C.P., Heuzenroeder M.W.,
 RA "Genomic structure of the Salmonella enterica serovar Typhimurium DT
 RT 64 bacteriophage ST64T: evidence for modular genetic architecture."
 RL J. Bacteriol. 185:3473-3475 (2003).
 DR EMBL: AY052766; AAL15520.1; -
 DR SEQUENCE 118 AA; 12875 MW; AB45EFC6A80C8C CRC64;

Query Match 1.3%; Score 7; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 LFKDQV 313
 |||||
 DB 82 LFKDQV 88

RESULT 47

08CU33 PRELIMINARY; PRT; 120 AA.
 AC 08CU33;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypoetical.
 GN OrderedlocusNames=y2310;
 OS Yersinia pestis.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Yersinia.
 OC NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G., III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., V.,
 RA Peterson J.D., Lindler L.B., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Niles W.L., Watson J.S., Blattner F.R.,
 RA Perry R.D.,
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611 (2002).
 DR EMBL: AE013833; AAM95869.1; -
 DR GO: GO:0003824; P:aromatic activity; IEA.
 DR GO: GO:0006725; P:aromatic compound metabolism; IEA.
 DR InterPro: IPR003779; CMD.
 DR Pfam: PF02627; CMD; 1.
 DR Hypoetical protein.
 DR SEQUENCE 120 AA; 13320 MW; 7DF4DADA5DE5A56 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRSHRL 32
 |||||
 DB 72 LRSHRL 78

RESULT 48

08CU9 PRELIMINARY; PRT; 123 AA.
 AC 08CU9;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Mus musculus 15 days embryo brain cDNA, RIKEN full-length enriched
 DE library, clone:G630024G08 product:hypothetical protein, full insert
 DE sequence.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Komori H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Komori H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Smiti N., Ishii Y., Nakamura S., Hazama M., Nishire T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Itoe K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Aachin U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imctani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Komori H., Kouda M., Koya S.,
 RA Kishihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Onosato N., Sano H.,
 RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: ACO90243; BAC41145.1;
 DR GO: GO:0016020; Cimetidine; IEA.
 DR InterPro: IPR005052; Lectin leg.
 DR Pfam: PF03368; Lectin_leg-Ilike; 1.
 DR Hypothetical protein.
 KW SEQUENCE 123 AA; 13394 MW; DF3FCB1E921895B CRC64;

Query Match 1.3%; Score 7; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 430 HRPFPs 436
 DB 113 HRPFPs 119

RESULT 49
 ID Q81RB0 PRELIMINARY; PRT; 125 AA.
 AC Q81RB0; Q6H213; Q6XTH3;
 DT 01-JUN-2003 (TREMblrel. 24, Created)
 DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
 DT 01-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE Conserved domain protein.
 GN Ordered locus names=BAC2140, BAS1992; ORFNames=GBA2140;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Ballile L.W., Paulsen I.T.,
 RA Nelson K.E., Tettein H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
 RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA Debey R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson U.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plant R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RT "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
 RL Nature 423:81-86(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Frazer C.M.;
 RT "Bacillus anthracis comparative genomics";
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sterne;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Kelm P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE017030; AAP26024.1;
 DR EMBL: AE017334; AAT31258.2;
 DR EMBL: AE017225; AAT54306.1;
 DR TIGR: BA2140;
 DR InterPro: IPR002110; ANK.
 DR PRINTS: PRO1415; ANKYRIN.
 KW SEQUENCE 125 AA; 14820 MW; FA4489EE44E89B35 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 68 IVSGDLI 74
 DB 9 IVSGDLI 15
 RESULT 50
 ID AAT31258 PRELIMINARY; PRT; 125 AA.
 AC AAT31258;
 DT 01-JUN-2004 (TREMblrel. 27, Created)
 DT 01-JUN-2004 (TREMblrel. 27, Last sequence update)
 DT 01-JUN-2004 (TREMblrel. 27, Last annotation update)
 DE Conserved domain protein.
 GN GBA2140.
 OS Bacillus anthracis str. Ames 0581.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group; Bacillus anthracis.
 OX NCBI_TaxID=261594;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S., Fraser C.M.,
 RT "Bacillus anthracis comparative genomics";
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017334; AAT31258.2; -
 SQ SEQUENCE 125 AA; 14820 MW; FA4489EB4458935 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2.3e-02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 IVSGDLI 74
 Db 9 IVSGDLI 15

RESULT 51
 SSB2_STRAS STANDARD; PRT; 131 AA.
 ID SSB2_STRAS
 AC 08E7H6;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Single-strand binding protein 2 (SSB 2) (Helix-destabilizing protein 2).
 GN Name=ssb2; OrderedLocNames=gbs0178;
 GN Streptococcus agalactiae (serotype III).
 OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216495;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEM316 / Serotype III;
 RA MEDLINE=22242508; PubMed=12354221;
 RA Glaser P., Rusnok C., Buchrieser C., Chevallier F., Frangoul L.,
 RA Masdek T., Zouine M., Couve E., Lallouf L., Poyart C., Trieu-Cuot P.,
 RA Kunst F.;
 RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
 RT invasive neonatal disease.";
 RL Mol. Microbiol. 45:1499-1513(2002).
 CC -1- FUNCTION: This protein is essential for replication of the
 CC chromosome. It is also involved in DNA recombination and repair
 CC (by similarity).
 CC -1- SIMILARITY: Contains 1 SSB domain.

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 CC
 CC EMBL; AL766844; CAD45823.1; -
 DR HSSP; P02339; IEYG.
 DR Sagaliet; gbs0178; -
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR InterPro; IPR00424; SSB_protein.
 DR InterPro; IPR010913; SS_Binding.
 DR Pfam; PF00436; SSB; 1.
 DR TIGRFAMs; TIGR00621; ssb; 1.
 DR PROSITE; PS50935; SSB; 1.
 KM Complete proteome; DNA repair; DNA replication; DNA-binding.
 FT DOMAIN 1 103 SSB.
 SQ SEQUENCE 131 AA; 14791 MW; 447B06B0420411DD CRC64;

Query Match 1.3%; Score 7; DB 1; Length 131;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 61 ETLASYG 67
 Db 59 ETLASYG 65

RESULT 52
 SSB2_STRAS STANDARD; PRT; 131 AA.
 ID SSB2_STRAS
 AC 08E220;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Single-strand binding protein 2 (SSB 2) (Helix-destabilizing protein 2).
 GN Name=ssb2; OrderedLocNames=SAG0180;
 GN Streptococcus agalactiae (serotype V).
 OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RA MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
 RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Federova N.B., Scanlan D., Khouli H.M., Mulligan S.,
 RA Carey H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Tacchini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
 RA Rinaldo D., Rappelli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V Streptococcus agalactiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
 CC -1- FUNCTION: This protein is essential for replication of the
 CC chromosome. It is also involved in DNA recombination and repair
 CC (by similarity).
 CC -1- SIMILARITY: Contains 1 SSB domain.

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 CC
 CC EMBL; AE014200; AAM99087.1; -
 DR HSSP; P02339; IEYG.
 DR TIGR; SAG0180;
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR InterPro; IPR00424; SSB_protein.
 DR InterPro; IPR010913; SS_Binding.
 DR Pfam; PF00436; SSB; 1.
 DR TIGRFAMs; TIGR00621; ssb; 1.
 DR PROSITE; PS50935; SSB; 1.
 KM Complete proteome; DNA repair; DNA replication; DNA-binding.
 FT DOMAIN 1 103 SSB.
 SQ SEQUENCE 131 AA; 14775 MW; 5204E89D421B0EDD CRC64;

Query Match 1.3%; Score 7; DB 1; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 61 ETLASYG 67
 Db 59 ETLASYG 65

RESULT 53
 Q8ZE27 PRELIMINARY; PRT; 140 AA.
 AC Q8ZE27; Q74U89;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE Putative decarboxylase (EC 4.1.1.44).
 GN OrderedLocustNames=YPL846, YPO1999;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 NCBI_TaxID=632;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
 RA Parkhill J., Wren B.W., Thomson N.R., Tlball R.M., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Pelletier T., Hamlin N., Holroyd S., Jagsels K., Karlyshay A.V.,
 RA Leather S., Mouton S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,
 RA "genome sequence of Yersinia pestis, the causative agent of plague.",
 RT Nature 413:523-527(2001).
 RL Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=91001 / Biovar Mediaevalis;
 RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
 RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
 RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
 RA Yang R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ014151; CAC90812.1; -
 DR EMBL; AE017134; AAC62066.1; -
 DR PIR; AH0243; AH0243.
 DR GO; GO:0047575; F:4-carboxymuconolactone decarboxylase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006725; P:anabolic compound metabolism; IEA.
 DR InterPro; IPR003779; CMD.
 DR Pfam; PF02627; CMD.
 KW Complete proteome; Lyase.
 SQ SEQUENCE 140 AA; 15578 MW; 6519E30B5B7DC060 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred.No.2.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 26 LRSHRL 32
 DB 92 LRSHRL 98
 RESULT 54
 AAS62066 PRELIMINARY; PRT; 140 AA.
 ID AAS62066;
 AC AAS62066;
 DT 24-MAR-2004 (TREMblrel. 27, Created)
 DT 24-MAR-2004 (TREMblrel. 27, Last sequence update)
 DT 04-MAY-2004 (TREMblrel. 27, Last annotation update)
 DE Putative decarboxylase.
 GN YPL846;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 NCBI_TaxID=632;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=91001 / Biovar Mediaevalis;
 RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
 RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
 RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,

RA Yang R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017134; AAC62066.1; -
 SQ SEQUENCE 140 AA; 15578 MW; 6519E30B5B7DC060 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred.No.2.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 26 LRSHRL 32
 DB 92 LRSHRL 98
 RESULT 55
 Q973V4 PRELIMINARY; PRT; 141 AA.
 ID Q973V4;
 AC Q973V4;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Hypothetical protein ST0794.
 GN OrderedLocustNames=ST0794;
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 NCBI_TaxID=11955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine Y., Baba S.-I., Ankel A., Kosugi H., Hosoeyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermocacidophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain 7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL; AP000983; BAB5806.1; -
 DR HSSP; Q9W282; 103U.
 DR InterPro; IPR007842; HEPN.
 DR Pfam; PF05168; HEPN.1.
 DR SMART; SM00748; HEPN.1.
 DR PROSITE; PS50910; HEPN.1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 141 AA; 16604 MW; 524D8D3EB9ABF1BF CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred.No.2.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 RVRLLKR 10
 DB 5 RVRLLKR 11
 RESULT 56
 Q8C938 PRELIMINARY; PRT; 141 AA.
 ID Q8C938;
 AC Q8C938;
 DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 DE enriched library, clone:AV30050C11 product:hypothetical protein, full
 DE insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=9279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA The FANTOM Consortium;
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sakaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Harada A.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Obara B., Natsukawa M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX Adachi U., Aizawa K., Akimura T., Aizawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saio R., Saichou H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tomaru A., Takahashi F., Takaku-Akashi S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK043043; BAC31446.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 141 AA; 15822 MW; A93B86C1DC73D05 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 IPSSTDs 93
 DB 117 IPSSTDs 123

RESULT 57

Q6XIE4
 ID Q6XIE4 PRELIMINARY; PRT; 144 AA.
 AC Q6XIE4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Similar to Drosophila melanogaster CG1686 (Frigment).
 OS Drosophila yakuba (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887302; PubMed=14525923;
 RA Domazet-Loso T., Tautz D.;
 RT "An evolutionary analysis of orphan genes in Drosophila";
 RL Genome Res. 13:2213-2219(2003).
 DR EMBL: AY231886; AAR09909.1; -
 DR InterPro: IPR004274; NIF.
 DR Pfam: PF03031; NIF; 1.
 DR SMART: SMO0577; CPDC; 1.
 FT NON_TER 1
 FT NON_TER 144
 SQ SEQUENCE 144 AA; 16871 MW; BB0790DFAB8DE3E CRC64;

Query Match 1.3%; Score 7; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 DYRSYLS 354
 DB 129 DYRSYLS 135

RESULT 58
 Q8ABF0
 ID Q8ABF0 PRELIMINARY; PRT; 144 AA.
 AC Q8ABF0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 DE OrderedLocustNames=Br0160;
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 NCBI_TaxID=818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VP1-5482 / ATCC 29148;
 RX MEDLINE=2250858; PubMed=1263928;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis";
 RL Science 299:2074-2076(2003).
 DR EMBL: AE016926; AA075267.1; -
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 144 AA; 16994 MW; 1502B6F45A0363A3 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 LLPESFI 285
 DB 107 LLPESFI 113

RESULT 59
 AAR09909 PRELIMINARY; PRT; 144 AA.
 AC AAR09909;

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DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Similar to Drosophila melanogaster CG1696 (Fragment).
OS Drosophila yakuba (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RX NCBI_TaxID=7245;
RP SEQUENCE FROM N.A.
RX MEDLINE=22887302; PubMed=14525923;
RA Domazet-Lozo T., Tautz D.;
RL "An evolutionary analysis of orphan genes in Drosophila.";
DR EMBL; AY231886; AAR09909.1; -.
FT NON_TER 1
SQ SEQUENCE 144 AA; 16871 MW; BE0790DFAEBDE3E CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 144;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 DVSRLVS 354
DB 129 DVRSVLS 135

RESULT 60
Q8GDK1
ID Q8GDK1 PRELIMINARY; PRT; 148 AA.
AC Q8GDK1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Orf20.
GN Name=orf20;
OS Photobacterium luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photobacterium.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WT4;
RX MEDLINE=22454990; PubMed=12564983;
RA Waterfield N.R., Daborn P.J., Ffrench-Constant R.H.;
RT "Genomic islands in Photobacterium";
RL Trends Microbiol. 10:541-545(2002).
DR EMBL; AY144118; AAN64224.1; -.
DR InterPro; IPR009063; Bac_Ig/alb_bind.
DR InterPro; IPR007048; GPM_gp25.
DR Pfam; PF04965; GPM_gp25; 1.
SQ SEQUENCE 148 AA; 16800 MW; 8C3B338A167BC3B3 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 148;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 SIQDNNAH 156
DB 21 SIQDNNAH 27

RESULT 61
Q94173
ID Q94173 PRELIMINARY; PRT; 149 AA.
AC Q94173;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein OSJNBa0010P20.21.
GN Name=OSJNBa0010P20.21;

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OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX Huang E.N., de la Bastide M., Vil D.M., Preston R.R., Spiegel L.A.,
RA See L.H., Shah R., Matero A., O'Shaughnessy A., Rodriguez M.,
RA Shekter M., Swaby I., Schutz K., Habermann K., Parnell L.D.,
RA Nascimben L.U., Dedhia N.N., McCombie W.R.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC011806; AAK53844.1; -.
DR Gramene; Q94173; -.
KW Hypothetical protein.
SQ SEQUENCE 149 AA; 15279 MW; 6E8B7E6B653DF64 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 149;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 RPPFRPS 510
DB 86 RPPFRPS 92

RESULT 62
YA87_MYCN
ID YA87_MYCN STANDARD; PRT; 150 AA.
AC P75606;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein MPR087 (R02_orf150).
GN OrderedLocustNames=MPN087; ORFNames=MP068;
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelfeich R., Hilbert H., Pliagens H., Pirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: TO THE CENTRAL SECTION OF M.PNEUMONIAE MPR085.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sb-sib.ch).
DR EMBL; AE000009; AAB95716.1; -.
DR PIR; S73394; S73394.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 48
FT TRANSMEM 68
FT TRANSMEM 89
FT TRANSMEM 109
FT TRANSMEM 123
FT TRANSMEM 143
FT TRANSMEM 150
SQ SEQUENCE 150 AA; 17549 MW; FF60FF60C08803B2 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 150;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 DVFGLVV 334
DB 94 DVFGLVV 100

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RESULT 63
Q93VE4 PRELIMINARY; PRT; 151 AA.
ID Q93VE4;
AC Q93VE4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE P0560B06.34 protein (P0043B10.26 protein).
GN Name=P0560B06.34; Synonyms=P0043B10.26;
OS Oryza sativa (japonica cultivar-group);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriodes; Oryzae; Oryza.
OC NCBI_TaxID=39947;
CX RN
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karsawa M., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizunayashi T., Mukai Y.,
RA Nagaoka H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Nishikawa T., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003281; BAB64766.1; -
DR EMBL; AP003281; BAB64766.1; -
DR Gramene; Q93VE4; -
SQ SEQUENCE 151 AA; 15482 MW; C7FE32E38A4657 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 151;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 RPPRPS 510
Db 88 RPPRPS 94

RESULT 64
Q7X9T7 PRELIMINARY; PRT; 152 AA.
ID Q7X9T7;
AC Q7X9T7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gbss1-1 protein (Fragment).
GN Name=gbss1-1;
OS Geum rivale;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Rosales; Rosaceae; Rosoideae; Geum.
OC NCBI_TaxID=148897;
CX RN
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22660791; PubMed=12775526;
RA Smedmark U.E.B., Eriksson T., Evans R.C., Campbell C.S.;
RA "Ancient allopolyploid speciation in Geinae (Rosaceae): evidence from
RA nuclear granule-bound starch synthase (GBSSI) gene sequences.";
RL Syst. Biol. 52:374-385(2003).
DR EMBL; AF534201; CAD59468.1; -
FT NON TER 1 152 1
FT NON TER 152 152 1
SQ SEQUENCE 152 AA; 17276 MW; 1B8E4AAC9B005FB CRC64;

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Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 152;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 LRLSLIC 36
Db 90 LRLSLIC 96

RESULT 65
P9AA ANACY STANDARD; PRT; 160 AA.
ID P9AA ANACY
AC P07325;
DT 01-APR-1998 (Rel. 07, Created)
DT 01-APR-1998 (Rel. 07, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Allophycocyanin alpha chain.
GN Name=apca;
OS Anabaena cylindrica.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OC NCBI_TaxID=1165;
CX RN
RN [1]
RP SEQUENCE.
RA Minami Y., Yamada F., Hase T., Matsubara H., Murakami A., Fujita Y.,
RA Takeo T., Shimonishi Y.;
RT "Amino acid sequences of allophycocyanin alpha- and beta-subunits
RT isolated from Anabaena cylindrica.";
RL FEBS Lett. 191:216-220(1985).
CC -1- FUNCTION: Light-harvesting photosynthetic bile pigment-protein
CC from the phycobiliprotein complex. Allophycocyanin has a maximum
CC absorption at approximately 650 nanometers.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -1- PTM: Contains one covalently linked bilin chromophore.
CC -1- SIMILARITY: Belongs to the phycobiliprotein family.
DR PIR; A24224; AFALAC.
DR HSSP; P00315; 1B33.
DR InterPro; IPR009050; Globin like.
DR InterPro; IPR001659; Phycobilisome.
DR Pfam; PF00502; Phycobilisome; 1.
DR Pfam; PF000340; Phycobilisome; 1.
KW Bile pigment; Direct protein sequencing; Electron transport;
KW Photosynthesis; Phycobilisome.
FT BINDING 80 80 Phycocyanobilin chromophore.
SQ SEQUENCE 160 AA; 17081 MW; 537C408172597624 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 160;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YGIYSGD 72
Db 93 YGIYSGD 99

RESULT 66
P9AA_FREDI STANDARD; PRT; 160 AA.
ID P9AA_FREDI
AC P16570;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Allophycocyanin alpha chain 1.
GN Name=apca;
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
OC NCBI_TaxID=1197;
CX RN
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89053869; PubMed=2461358;
RA Hounard J., Capuano V., Courain T., Tandeau de Marsac N.;
RA "Genes encoding core components of the phycobilisome in the
RA cyanobacterium Calothrix sp. strain PCC 7601: occurrence of a

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RT multigene family."
RL J. Bacteriol. 170:5512-5521(1988).
CC -1- FUNCTION: Light-harvesting photosynthetic bile pigment-protein
CC from the phycobiliprotein complex. Allophycocyanin has a maximum
CC absorption at approximately 650 nanometers.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -1- PTM: Contains one covalently linked bilin chromophore.
CC -1- SIMILARITY: Belongs to the phycobiliprotein family.
CC -----
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CC -----
DR EMBL: M20806; AA24874.1; -.
DR HGSP: P00315; 1B33.
DR InterPro: IPR009050; Globin-like.
DR InterPro: IPR001659; Phycobillism.
DR Pfam: PF00502; Phycobillism; 1.
DR ProDom: PD000340; Phycobillism; 1.
KM Bile pigment; Electron transport; Photosynthesis; Phycobillism.
FT INIT MET 0
FT BINDING 80 80 Phycocyanobilin chromophore.
SQ SEQUENCE 160 AA; 17233 MW; 9C6E55F6A4923C29 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YGIVSGD 72
DB 93 YGIVSGD 99

RESULT 67
PHAA_PORYE STANDARD; PRT; 160 AA.
ID PHAA_PORYE
AC P59856;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Allophycocyanin alpha chain.
GN Name:apca;
OS Porphyra yezoensis.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
OX NCBI_TaxID=2788;
[1]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99287890; Pubmed=10358042;
RA Liu J.Y., Jiang T., Zhang J.P., Liang D.C.;
RT "Crystal structure of allophycocyanin from red algae Porphyra
RL yezoensis at 2.2-A resolution."
J. Biol. Chem. 274:16945-16952(1999).
CC -1- FUNCTION: Light-harvesting photosynthetic bile pigment-protein
CC from the phycobiliprotein complex. Allophycocyanin has a maximum
CC absorption at approximately 650 nanometers.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -1- PTM: Contains one covalently linked bilin chromophore.
CC -1- SIMILARITY: Belongs to the phycobiliprotein family.
CC -1- PDB: 1KN1; X-ray; A=1-160.
DR InterPro: IPR001659; Phycobillism.
DR Pfam: PF00502; Phycobillism; 1.
DR ProDom: PD000340; Phycobillism; 1.
KM 3D-structure; Bile pigment; Chloroplast; Electron transport;
FT Photosynthesis; Phycobillism.
FT INIT MET 0
FT BINDING 80 80 Phycocyanobilin chromophore.
SQ SEQUENCE 160 AA; 17366 MW; 4CC4B78D67B2B3D CRC64;

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Query Match 1.3%; Score 7; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YGIVSGD 72
DB 93 YGIVSGD 99

RESULT 68
Q8DU53 PRELIMINARY; PRT; 160 AA.
ID Q8DU53;
AC Q8DU53;
DT 01-MAR-2003 (TRIMBLrel. 23, Created)
DT 01-MAR-2003 (TRIMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRIMBLrel. 26, Last annotation update)
DE Putative transcriptional regulator protein.
GN Putative transcriptionsal regulator protein.
OS Streptococcus mutans.
OC Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAI59 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; Pubmed=12397186; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RA Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UAI59, a cariogenic dental
RT pathogen."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC -1- SIMILARITY: Contains 1 HTH marv-type DNA-binding domain.
DR EMBL: AB014947; AAN58794.1; -.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000835; HTH_MaRR.
DR InterPro: IPR009058; wing_hlx_DNA_bnd.
DR Pfam: PF01047; MaRR; 1.
DR SMART: SM00347; HTH_MaRR; 1.
SQ Complete proteome: DNA-binding; Transcription regulation.
SQ SEQUENCE 160 AA; 18693 MW; 094B79A612C122A CRC64;

Query Match 1.3%; Score 7; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 VYNATLK 266
DB 64 VYNATLK 70

RESULT 69
Q96MMO PRELIMINARY; PRT; 163 AA.
ID Q96MMO;
AC Q96MMO;
DT 01-DEC-2001 (TRIMBLrel. 19, Created)
DT 01-DEC-2001 (TRIMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TRIMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ32172.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX Pubmed=14702039;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

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RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahashi K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuna M., Shiratori A.,
 RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Nishimura K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimura M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nemura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Matsuhashi K., Yuhki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujitawa T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohnoiri Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
 RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shitai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs." ;
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL, AK056734, BAB1267.1 ;
 SQ SEQUENCE 163 AA; 18797 MW; B69B19F5FC0E1A07 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 163;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 321 RQALNLP 327
 Db 4 RQALNLP 10

RESULT 70
 Q70IG5 PRELIMINARY; PRT; 166 AA.
 AC Q70IG5;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 GN AGCP3440 (Fragment).
 GN Name=agcG54193; ORFNames=ENSANG0000010761;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
 OC NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RL Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAA01008807; EAA04291.1 ;
 DR GO: GO:0042302; F: structural constituent of cuticle; IEA.
 DR InterPro; IPR000618; Insect_cuticle.
 DR Pfam; PF00379; Cuticn_bind_4; 1.
 DR PRINTS; PR00947; CUTICLE.
 DR PROSITE; PS00233; CUTICLE; UNKNOWN_1.
 RT NON TER
 SQ SEQUENCE 166 AA; 18911 MW; 95E3773EDD2F781D CRC64;

Query Match 1.3%; Score 7; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 KDPLTGD 59
 Db 78 KDPLTGD 84

RESULT 71
 Q864L5 PRELIMINARY; PRT; 166 AA.
 AC Q864L5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 DE Ordered locus names=B13164;
 OS Bifidobacterium longum.
 OC Bacteria; Actinobacteriae; Bifidobacteriales;
 OC Bifidobacteriaceae; Bifidobacterium.
 OC NCBI_TaxID=216816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCC 2705;
 RX MEDLINE=22294977; PubMed=12381787;
 RA Schell M.A., Karmaliantzou M., Snel B., Vilanova D., Berger B.,
 RA Fessl G., Zwielen W.-C., Desiere F., Bork P., Delley M.,
 RA Pridmore R.D., Arigoni F.,
 RT "The genome sequence of Bifidobacterium longum reflects its adaptation
 RT to the human gastrointestinal tract." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
 DR EMBL; AE014766; AAN25164.1 ;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 166 AA; 17619 MW; 863A301DD8DBAE2D CRC64;

Query Match 1.3%; Score 7; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 515 TDGRLSF 521
 Db 59 TDGRLSF 65

RESULT 72
 Q97H82 PRELIMINARY; PRT; 167 AA.
 AC Q97H82;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein CAC2131.
 GN Ordered locus names=CAC2131;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OC NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RX DOI=10.1128/JB.185.16.4623-4638.2001;
 RA Noelling U., Breton G., Ometchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hilti J., Wolf Y.I.,
 RA Tatunov R.L., Sabathe F., Doucette-Stamm J.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.,
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum." ;
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL; AE007714; AAK80089.1 ;
 DR PIR; F97162; F97162.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 167 AA; 19373 MW; 386752F8386ED78 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 339 LKLRIR 345
Db 103 LKLRIR 109

RESULT 73

QYV177 PRELIMINARY; PRT; 170 AA.
ID QYV177;
AC QYV177;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Glutathione peroxidase (EC 1.11.1.9).
GN OrderedAccession=PM1006;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcales;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2825696; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Lartner F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Algren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Arellano A., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinner E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation."
RL Nature 424:1042-1047(2003).
CC - SIMILARITY: Belongs to the glutathione peroxidase family.
DR EMBL; BX572092; CAB19465.1; -
DR GO; GO:0004602; F:glutathione peroxidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR GO; GO:0006979; F:response to oxidative stress; IEA.
DR InterPro; IPR000889; Glut_peroxidase.
DR Pfam; PF00255; GSHpx; 1.
DR PROSITE; PS00460; GLUTATHIONE PEROXID 1; 1.
KM Complete proteome; Oxidoreductase; Peroxidase.
SQ SEQUENCE 170 AA; 18947 MW; 83189938CED621F CRC64;
Query Match 1.3%; Score 7; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 298 YKDLQKL 304
Db 54 YKDLQKL 60

RESULT 74

Q8T018 PRELIMINARY; PRT; 172 AA.
ID Q8T018
AC Q8T018;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE GH27769P.
GN ORFNames=CG9619;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Eurytomidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Chapleton M., Brokstein P., Hong L., Agayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
RA Gonzalez W., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nunoo J., Paclieb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY069230; AL39375.1; -
DR FlyBase; FBgn0036862; CG9619.
DR InterPro; IPR005036; CEM_21.
DR Pfam; PF03370; CEM_21; 1.
SQ SEQUENCE 172 AA; 18713 MW; FE0D1923C2A3F6F3 CRC64;

Query Match

1.3%; Score 7; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 415 LPSTHT 421
Db 125 LPSTHT 131

RESULT 75

Q7XJ34 PRELIMINARY; PRT; 182 AA.
ID Q7XJ34
AC Q7XJ34;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Dechloratad1 (Fragment).
OS Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=51351;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=leaf;
RA Tang H.S., Hur Y.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY34835; AAP92379.1; -
FT NON_TER 182
FT NON_TER 182
SQ SEQUENCE 182 AA; 21273 MW; 2C47973EB9C7F5BC CRC64;
Query Match 1.3%; Score 7; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 382 DNTVRVQ 388
Db 150 DNTVRVQ 156

Search completed: November 16, 2004, 07:30:56
Job time : 202 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:13:20 ; Search time 155 Seconds
(without alignments)
1208.108 Million cell updates/sec

Title: US-09-927-458-2

Sequence: 1 MRLRVRLKRWLPLEPETE.....DRFPRPSRGHPTDRLSFM 522

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	490	93.9	522	6	ADAs7283 Human sec
2	490	93.9	522	6	ADAs1153 Human sec
3	490	93.9	522	6	ABR47958 Human sec
4	490	93.9	522	7	ADCT74366 Human sec
5	417	79.9	522	2	AAW68521 Human RLP
6	389	74.5	591	4	AAAB35161 Human SXP
7	354	67.8	607	4	AAU32109 Novel hum
8	330	63.2	443	4	AAAB35160 Human SXP
9	271	51.9	317	5	ABR90108 Human pol
10	231	44.3	231	7	ADJ68946 Human hea
11	200	38.3	221	6	ADAs4155 Human pro
12	200	38.3	462	5	ABR90109 Human pol
13	200	38.3	462	6	ADAs7586 Human sec
14	200	38.3	462	6	ADAs41482 Human sec
15	200	38.3	462	6	ABR48139 Human sec
16	200	38.3	462	6	ADCT4596 Human sec
17	134	25.7	549	4	ABG18510 Novel hum
18	134	25.7	549	4	ABG18510 Novel hum
19	128	24.5	174	6	ADAs7587 Human sec
20	128	24.5	174	6	ADAs41483 Human sec
21	128	24.5	174	6	ABR48140 Human sec
22	128	24.5	174	6	ADCT4597 Human sec
23	86	16.5	482	3	AAV41397 Human sec
24	86	16.5	482	3	AAV83047 F-box pro
25	76	14.6	76	8	ABO54274 Human gen

26	63	12.1	94	4	AAU32107	AAU32107 Novel hum
27	59	11.3	113	3	AAV87356	AAV87356 Human sig
28	53	10.2	225	4	ABG06838	ABG06838 Novel hum
29	47	9.0	47	8	ABO59862	ABO59862 Human gen
30	39	7.5	39	3	AAV83054	AAV83054 F-box mot
31	39	7.5	39	3	AAO22459	AAO22459 Human F-b
32	38	7.3	38	2	AAV02272	AAV02272 A F-box p
33	38	7.3	38	4	AAE08044	AAE08044 Human F-b
34	38	7.3	38	7	AAE39652	AAE39652 Human F-b
35	32	6.1	53	4	ABG18509	ABG18509 Novel hum
36	32	6.1	53	4	AAU32108	AAU32108 Novel hum
37	32	2.9	38	2	AAV02272	AAV02272 A F-box p
38	38	2.9	38	4	AAE08045	AAE08045 Human F-b
39	15	2.9	38	7	AAE39653	AAE39653 Mouse F-b
40	13	2.5	13	2	AAV41578	AAV41578 Fragment
41	13	2.5	13	2	AAV41577	AAV41577 Fragment
42	8	1.5	57	4	AAAG94240	AAAG94240 Human rep
43	8	1.5	63	8	ABO5854	ABO5854 Human gen
44	8	1.5	92	5	ABP10900	ABP10900 Human ORF
45	8	1.5	183	4	AAU5117	AAU5117 Proponib
46	8	1.5	183	6	ABM51636	ABM51636 Proponib
47	8	1.5	572	3	AAAG32036	AAAG32036 Arabidops
48	8	1.5	628	4	AAAG66450	AAAG66450 Murine be
49	8	1.5	789	6	ABU21326	ABU21326 Protein e
50	50	1.3	13	7	ADCS4146	ADCS4146 Peptide 1
51	51	1.3	20	2	AAV72285	AAV72285 Glutamic
52	52	1.3	20	3	AAV59556	AAV59556 GAD65 fra
53	52	1.3	26	7	ADCS4148	ADCS4148 Peptide 1
54	54	1.3	32	7	ADM08067	ADM08067 Canine im
55	55	1.3	32	7	ADM07905	ADM07905 Canine im
56	56	1.3	32	7	ADM08430	ADM08430 Canine im
57	57	1.3	32	7	ADM08438	ADM08438 Canine im
58	59	1.3	32	7	ADM07907	ADM07907 Canine im
59	60	1.3	32	7	ADM07904	ADM07904 Canine im
60	61	1.3	32	7	ADM08347	ADM08347 Canine im
61	62	1.3	32	7	ADM08348	ADM08348 Canine im
62	63	1.3	32	7	ADM08442	ADM08442 Canine im
63	64	1.3	32	7	ADM07910	ADM07910 Canine im
64	65	1.3	32	7	ADM08438	ADM08438 Canine im
65	66	1.3	32	7	ADM08062	ADM08062 Canine im
66	67	1.3	32	7	ADM08336	ADM08336 Canine im
67	68	1.3	58	6	ADAs7203	ADAs7203 Human sec
68	69	1.3	58	6	ADAs41080	ADAs41080 Human sec
69	70	1.3	58	6	ABR47918	ABR47918 Human sec
70	71	1.3	59	2	AAV36325	AAV36325 Human sec
71	72	1.3	59	3	AAV73500	AAV73500 Human sec
72	73	1.3	59	6	ADAl1698	ADAl1698 Human nov
73	74	1.3	63	6	ABP55962	ABP55962 Manduca s
74	75	1.3	64	6	ABP55961	ABP55961 Manduca s
75	76	1.3	64	6	AAU42520	AAU42520 Proponib
76	77	1.3	64	6	ABM39039	ABM39039 Proponib
77	78	1.3	65	4	AAU18916	AAU18916 Novel pro
78	79	1.3	65	4	AAV86229	AAV86229 Human rep
79	79	1.3	66	4	AAU50836	AAU50836 Proponib
80	80	1.3	66	6	ABM47355	ABM47355 Proponib
81	81	1.3	76	6	AAU39531	AAU39531 Proponib
82	82	1.3	76	6	ABM36050	ABM36050 Proponib
83	84	1.3	83	3	AAU03130	AAU03130 Human sec
84	85	1.3	89	4	AAU18904	AAU18904 Peptide #
85	86	1.3	89	4	ABR38029	ABR38029 Peptide #
86	87	1.3	89	4	AAV31445	AAV31445 Peptide #
87	88	1.3	89	4	ABR23262	ABR23262 Protein #
88	88	1.3	89	4	AAU71164	AAU71164 Human Don
89	89	1.3	89	4	AAV58658	AAV58658 Human bra
90	90	1.3	89	5	ABG52876	ABG52876 Human liv
91	91	1.3	89	5	ABG40961	ABG40961 Human pep
92	92	1.3	90	8	ABO60647	ABO60647 Human gen
93	93	1.3	92	4	ABBI5782	ABBI5782 Human ner
94	95	1.3	93	4	AAU17900	AAU17900 Novel hum
95	96	1.3	93	6	ABU44049	ABU44049 Protein e
96	97	1.3	93	7	ADG41280	ADG41280 Human res
97	98	1.3	101	4	AAV95027	AAV95027 Human rep
98	98	1.3	101	4	AAV95027	AAV95027 Human rep

99 7 1.3 104 5 ADK34930
100 7 1.3 107 4 AAU45802

ADK34930 Novel hum
AAU45802 Propionib

ALIGNMENTS

RESULT 1

ADK57283
ID ADK57283 standard; protein; 522 AA.

AC ADK57283;

DT 20-NOV-2003 (first entry)

DE Human secreted protein #566.

XX immunosuppressive; antiinflammatory; antiasthmatic; anti-allergic;

KW cytoostatic; cerebroprotective; neuroprotective; neurotropic;

KW cardiovascular; antiarteriosclerotic; gene therapy;

KW human secreted protein; immune disorder; inflammation;

KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;

KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;

KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;

KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;

KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.

XX WO2002102994-A2.

XX 27-DEC-2002.

XX 19-MAR-2002; 2002WO-US008278.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI, 2003-167512/16.

XX N-PSDB; ADA56387.

XX New human secreted polypeptides and polynucleotides, useful for

XX diagnosing, treating or preventing e.g. immune disorders, inflammatory

XX conditions, respiratory disorders, cancers, CNS disorders, or

XX neurodegenerative disorders, or polypeptides comprising an amino acid

XX sequence at least 95% identical to the new sequences. The polypeptides,

XX antibodies or antibody fragments that bind to the polypeptides, nucleic

XX acids encoding the polypeptides, agonists or antagonists that binds to

XX the polypeptide, are useful in preparing diagnostic or pharmaceutical

XX compositions for diagnosing, treating or preventing an e.g. immune

XX disorders, inflammatory conditions (e.g. inflammatory bowel disease,

XX nephritis or Crohn's disease), respiratory disorders (e.g. asthma and

XX allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders

XX (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative

XX disorders (e.g. Parkinson's disease or Alzheimer's disease), and

XX cardiovascular disorders (e.g. atherosclerosis or myocarditis). The

XX polynucleotides are useful for chromosome identification, chromosome

XX mapping, for controlling gene expression through triple helix formation

XX or antisense DNA or RNA, in gene therapy, for identifying individuals

XX from minute biological samples, in forensic biology, and as hybridization

XX probes. The polypeptides are useful for as molecular weight markers on

CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)

CC gels, to raise antibodies, for testing biological activities, and for

CC treating or preventing neural disorders, immune system disorders,

CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,

CC renal, proliferative and/or cancerous diseases. This sequence corresponds

CC to one of the polypeptide of the invention. Note: The sequence data for

CC this patent did form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 522 AA;

Query Match 93.9%; Score 450; DB 6; Length 522;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLCTMGVSSNRTPTTNTYKDLTGDEETLASVGVSGDLICLLDIDPAPNPSSTD 92

DB 33 SLCTMGVSSNRTPTTNTYKDLTGDEETLASVGVSGDLICLLDIDPAPNPSSTD 92

QY 93 SEHSIIONNEQSLATSSNOTSMODEQSDSFOGQAQSGVWVNDMSMGPNFEASIQ 152

DB 93 SEHSIIONNEQSLATSSNOTSMODEQSDSFOGQAQSGVWVNDMSMGPNFEASIQ 152

QY 153 DNAMHAEAGTFPSPMLCSVESVEQVPHSLFTLYQSADCSNDALIVLHLMLESGY 212

DB 153 DNAMHAEAGTFPSPMLCSVESVEQVPHSLFTLYQSADCSNDALIVLHLMLESGY 212

QY 213 IPQTEAKALSMPEKMLSGVYKLOVHPLTEGSSATTCVPLGNLYVNAITKINNEIR 272

DB 213 IPQTEAKALSMPEKMLSGVYKLOVHPLTEGSSATTCVPLGNLYVNAITKINNEIR 272

QY 273 SVKRLQLLPESTICEKLGENVANTYKDLQKLSRLFKQOLVYPLLAFTROALNPVFG 332

DB 273 SVKRLQLLPESTICEKLGENVANTYKDLQKLSRLFKQOLVYPLLAFTROALNPVFG 332

QY 333 VVLPPELKLRIPLLDVAVSLASVACDLFTASNDPLMRFLYLRDPRDNTVAVOPD 392

DB 333 VVLPPELKLRIPLLDVAVSLASVACDLFTASNDPLMRFLYLRDPRDNTVAVOPD 392

QY 333 KELYKRKHIOKRESEKGFVNLPESTHTIPFPYNPPLMRPSSRLPGIIGGEYDQ 452

DB 333 KELYKRKHIOKRESEKGFVNLPESTHTIPFPYNPPLMRPSSRLPGIIGGEYDQ 452

QY 453 TLPIYGDPISSILPEPGTPOFPPLRPPVCPPLGPNPILTGRCGPNRPPRRP 512

DB 453 TLPIYGDPISSILPEPGTPOFPPLRPPVCPPLGPNPILTGRCGPNRPPRRP 512

QY 513 RPTDGRLSFM 522

DB 513 RPTDGRLSFM 522

RESULT 2

ADA41163

ID ADA41163 standard; protein; 522 AA.

AC ADA41163;

DT 20-NOV-2003 (first entry)

DE Human secreted protein.

XX Human; secreted protein; cancer; hyperproliferative disorder;

XX rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;

XX anaemia; allergic reaction; asthma; cardiovascular disorder;

XX wound healing; cytoostatic; immunosuppressive; neurotropic; neuroprotective;

XX antiviral; anti-allergic; hepatotropic; antidiabetic; anti-inflammatory;

XX vulnerable; candidate; gene therapy.

XX Homo sapiens.

XX WO2002102993-A2.

XX 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002MO-US008123.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI .Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-175238/17.
 XX
 PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.
 PS
 PS Claim 1; SEQ ID NO 1545; 3205bp; English.
 XX
 CC The invention relates to novel genes ADA39629-ADA40565 and proteins
 CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting,
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 CC thrombocytopenia), allergic reactions including asthma or eczema,
 CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 CC range restriction mapping, as molecular weight markers, or as
 CC hybridization or diagnostic probes. The polypeptides and antibodies are
 CC useful for providing immunological probes for differential identification
 CC of the tissues immunohistochemistry assays. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX
 SQ Sequence 522 AA;

Query Match 93.9%; Score 490; DB 6; Length 522;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLCTGYSNTRFTTLNWKDPLTGDERTIASYGVSGDLICLLIQDDIPRNPSSSD 92
 DB 33 SLCTGYSNTRFTTLNWKDPLTGDERTIASYGVSGDLICLLIQDDIPRNPSSSD 92
 QY 93 SEHSSTLQNNQEPPLATSSNOTSMQDQPSDSFGQAAGVWDDSMGLPSONFEAESIQ 152
 DB 93 SEHSSTLQNNQEPPLATSSNOTSMQDQPSDSFGQAAGVWDDSMGLPSONFEAESIQ 152
 QY 153 DNHMAEGCTFYSEPMGLCESSEYGVPSHLETLYSACCSDDANDLLYLHLMLESY 212
 DB 153 DNHMAEGCTFYSEPMGLCESSEYGVPSHLETLYSACCSDDANDLLYLHLMLESY 212
 QY 213 IPGTAKALSMPEKKLGSVYLLQYVMP.CEGSSATLTCVPLGNLIVNATLKINNEIR 272
 DB 213 IPGTAKALSMPEKKLGSVYLLQYVMP.CEGSSATLTCVPLGNLIVNATLKINNEIR 272

QY 273 SVKSLQLLPESFICEKLGENVANIYKLOKLSRLFKDOIYVPLAFTPOALNLPVFG 332
 DB 273 SVKSLQLLPESFICEKLGENVANIYKLOKLSRLFKDOIYVPLAFTPOALNLPVFG 332
 QY 333 VLPLELKLRTFRLLDVRSVLSAVCRDLPFTASNDPLMRFLYLRPDRNTVAVQTDW 392
 DB 333 VLPLELKLRTFRLLDVRSVLSAVCRDLPFTASNDPLMRFLYLRPDRNTVAVQTDW 392
 QY 393 KELYRKHIQKESPKGRFVWLPLPSSHTTTPFYENPLHPRPSPSRPDPGIGGEYQORP 452
 DB 393 KELYRKHIQKESPKGRFVWLPLPSSHTTTPFYENPLHPRPSPSRPDPGIGGEYQORP 452
 QY 453 TLPYVGDPISSLIPGPETPSQFPPLRPFRDPVGPLPBGPNILPGRGPNDRPFRPSRG 512
 DB 453 TLPYVGDPISSLIPGPETPSQFPPLRPFRDPVGPLPBGPNILPGRGPNDRPFRPSRG 512
 QY 513 RPTDGRUSFM 522
 DB 513 RPTDGRUSFM 522

RESULT 3

ID ABR47958 standard; protein, 522 AA.

ABR47958;

12-JUN-2003 (first entry)

Human secreted protein, SEQ ID 849.

Cardiac; antiarrhythmic; antiarteriosclerotic; vasotropic; cyrostatic;
 vulnerability; antiinflammatory; neurotropic; neuroprotective;
 antiparkinsonian; gene therapy; human; cardiovascular disorder.

Homo sapiens.

WO200295010-A2.

28-NOV-2002.

19-MAR-2002; 2002MO-US009785.

21-MAR-2001; 2001US-0277340P.

19-JUL-2001; 2001US-0306171P.

13-NOV-2001; 2001US-0331287P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM;

WPI; 2003-129429/12.

New human secreted proteins, useful for detecting, preventing,
 PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
 PT disorders such as arrhythmia.

Claim 13; SEQ ID NO 849; 1881bp; English.

The present invention relates to novel human secreted proteins (ABR47633-
 ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
 CC and their coding sequences are useful for the preparation of a diagnostic
 CC or pharmaceutical composition for diagnosing or treating a cardiovascular
 CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
 CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, renal disorders, for
 CC wound healing and epithelial cell proliferation, to treat inflammation or
 CC infection, for treating thrombosis and arteriosclerosis, for treating or
 CC preventing neural conditions which occurs in neuronal disorders or
 CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
 CC disease, to enhance bone and periodontal regeneration and aid in tissue


```

QY      393 KELYRKHIORKEGPKGRFVWLLPSSSTHTTIPFYNPNIHPRPPSSRLPGIIGGEYDQRP 452
D      393 KELYRKHIORKEGPKGRFVWLLPSSSTHTTIPFYNPNIHPRPPSSRLPGIIGGEYDQRP 452
QY      453 TLPVVGDPISSLIPGPGETPSQFPPLRRFPDVGPLPGPNPILPGRGGPNDRPFRPSRG 512
D      453 TLPVVGDPISSLIPGPGETPSQFPPLRRFPDVGPLPGPNPILPGRGGPNDRPFRPSRG 512
QY      513 RPTDGRLSFM 522
D      513 RPTDGRLSFM 522

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RESULT 5

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AAM68521
ID      AAM68521 standard; protein; 591 AA.

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AC      AAM68521;
XX
DT      25-JAN-1999 (first entry)
XX
DE      Human RIP-associated protein.
XX
KW      Human; RIP-associated protein; RAP; primer; PCR; amplification; probe;
KW      hybridisation; death domain; MORT MODULE; ICE-like family protease;
KW      kinase; TRAF domain; inflammation; cell death; tumour; HIV; infection.
XX
OS      Homo sapiens.
XX
PN      WO9841624-A1.
XX
PD      24-SEP-1998.
XX
PF      19-MAR-1998; 98MO-IL000125.
XX
PR      19-MAR-1997; 97IL-00120485.
XX
PA      (YEDA ) YEDA RES & DEV CO LTD.
XX
PI      Wallace D, Kovalenko A;
XX
DR      WPI, 1998-531565/45.
DR      N-PSDB; AAV57200.
XX
PT      DNA encoding RIP-associated protein (RAP) - useful for, e.g. treatment of
XX      tumour cells or HIV-infected cells.
XX
PS      Claim 10; Fig 2; 65bp; English.

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XX      This sequence represent part of a human RIP-associated protein (RAP). The
XX      coding sequence was isolated from a B-cell library by a yeast 2-hybrid
XX      screen using the RIP protein devoid of its "death domain" as a bait. The
XX      screen isolated a clone of about 1.9 kb. Primers were generated based on
XX      the sequence and used to PCR amplify probes for screening a colon and
XX      heart cDNA library. A further 300 bp of sequence was determined, which
XX      was added to the 1.9 kb of sequence from the B-cell library. The encoded
XX      protein does not contain a "death domain", MORT MODULE, ICE-like family
XX      protease domain, kinase domain, nor TRAF domains. RAP was shown to bind
XX      only to RIP and not to TRADD, MORT-1, p55-R, p75-R or MACH. The protein
XX      can be used to modulate or mediate RIP modulated/mediated intracellular
XX      effects on the inflammation, cell death or cell survival pathways in
XX      which RIP is involved, e.g. for treating tumour cells or HIV-infected
XX      cells.

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XX      Sequence 591 AA;

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QY      Query March      79.9%; Score 417; DB 2; Length 591;
      Best Local Similarity 100.0%; Pred. No. 0;
      Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      106 LATSNQTSMDQEPSDSFGQAAQSGVWVNDMSLGPSCNFEASIQDNAMAREGTGFP 165
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D      175 LATSNQTSMDQEPSDSFGQAAQSGVWVNDMSLGPSCNFEASIQDNAMAREGTGFP 234
QY      166 SEPMLCSSEVGEQVPHSLJETLYQSADCSGDANDALIVLTHLMLESQYIPQTEAKALSM 225
D      235 SEPMLCSSEVGEQVPHSLJETLYQSADCSGDANDALIVLTHLMLESQYIPQTEAKALSM 294
QY      226 EKMKLSGYTKIQYMHPLDEGSSATLTCTVPLGNLVYNTAKINNEIRSVKRLQLPESFI 285
D      225 EKMKLSGYTKIQYMHPLDEGSSATLTCTVPLGNLVYNTAKINNEIRSVKRLQLPESFI 354
QY      286 CEKLGENVANIYKDLQLSRLFKDQLYPLLAFTROALNPVFGVVLPLELKLRIFR 345
D      355 CEKLGENVANIYKDLQLSRLFKDQLYPLLAFTROALNPVFGVVLPLELKLRIFR 414
QY      346 LIDVRSVLSLAVCRDLFTASNDPLWRFVLRDPRDNTVAVQOTDMKELYRKXHIORKE 405
D      415 LIDVRSVLSLAVCRDLFTASNDPLWRFVLRDPRDNTVAVQOTDMKELYRKXHIORKE 474
QY      406 SPKGRFVWLLPSSSTHTTIPFYNPNIHPRPPSSRLPGIIGGEYDQRPFLPVGDPISSLI 465
D      475 SPKGRFVWLLPSSSTHTTIPFYNPNIHPRPPSSRLPGIIGGEYDQRPFLPVGDPISSLI 534
QY      466 PGPGETPSQFPPLRRFPDVGPLPGPNPILPGRGGPNDRPFRPSRGPTDGRLSFM 522
D      535 PGPGETPSQFPPLRRFPDVGPLPGPNPILPGRGGPNDRPFRPSRGPTDGRLSFM 591

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RESULT 6

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AAB35161
ID      AAB35161 standard; protein; 522 AA.

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AC      AAB35161;
XX
DT      09-APR-2001 (first entry)
XX
DE      Human Skp1-associated F-box protein-1 SAF-1beta SEQ ID NO: 10.
XX
KW      Human; protein degradation; slah-mediated degradation protein; SMDP;
KW      SCF-complex protein; SCP; slah-1alpha; slah-1 interacting protein; SIP;
KW      Skp1-associated F-box protein; SAF-1; SAF-2; SMD; cancer; cell division;
KW      Skp1-associated destruction-box protein; inflammatory disease.
XX
OS      Homo sapiens.
XX
PN      WO200077207-A2.
XX
PD      21-DEC-2000.
XX
PF      09-JUN-2000; 2000MO-US015873.
XX
PR      11-JUN-1999; 99US-0030517.
XX
PA      (BURN-) BURNHAM INST.
XX
PI      Reed JC, Matsuzawa S;
XX
DR      WPI; 2001-071273/08.
DR      N-PSDB; AAC67285.
XX
PT      Slah-Mediated Degradation Protein, useful for drug screening, for
XX      therapeutic applications and for functional genomics.
XX
PS      Claim 15; Page 107-108; 121bp; English.

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XX      The present invention provides the protein and coding sequences of
XX      several slah-mediated degradation proteins and SCF-complex proteins.
XX      These are designated slah-1alpha, slah-1 interacting protein (SIP),
XX      CC encodes two proteins due to alternative splicing (SIP-L and SIP-S). Skp1-
XX      associated F-box protein-1alpha and beta and -2 (SAF-1alpha, SAF-1beta
XX      and SAF-2) and Skp1-associated destruction-box protein (SMD). The
XX      proteins and their coding sequences are useful in the diagnosis and
XX      treatment of cancers, disorders where too little cell division occurs
XX      such as bone marrow aplasias, immunodeficiencies and inflammatory

```

CC diseases including sepsis, fibrosis, arthritis and graft versus host
 CC disease
 XX
 SQ Sequence 522 AA;
 Query Match 74.5%; Score 389; DB 4; Length 522;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 489; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 33 SLICTWGYSSNTRFTITLNYKDPPLTGDEETLASGYISGDLICILLODDIPAPNIPSSD 92
 DB 33 SLICTWGYSSNTRFTITLNYKDPPLTGDEETLASGYISGDLICILLODDIPAPNIPSSD 92
 QY 93 SEHSLSQNNNEPISLATSSNOTSMODEPSPDSFOGQAQSGVWDDSMIGSQNFABESIQ 152
 DB 93 SEHSLSQNNNEPISLATSSNOTSMODEPSPDSFOGQAQSGVWDDSMIGSQNFABESIQ 152
 QY 153 DNAMAEGTGFPSEPMKCSSEVGEQVPHSETLYQSGADSDANDALIVLHLMLESGY 212
 DB 153 DNAMAEGTGFPSEPMKCSSEVGEQVPHSETLYQSGADSDANDALIVLHLMLESGY 212
 QY 213 IPQGTAKALSMPEKMKLSGYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
 DB 213 IPQGTAKALSMPEKMKLSGYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
 QY 273 SVKRLQLLPESFTCKEKLGENVANITYKDLQKLSLTFDOLVYPLAFTROALNLPVFG 332
 DB 273 SVKRLQLLPESFTCKEKLGENVANITYKDLQKLSLTFDOLVYPLAFTROALNLPVFG 332
 QY 333 VVLPELKLRIFRLLDVRSVLSLSAVCRDLFTASNDPLMRFYLDRFNDTVRVDOTW 392
 DB 333 VVLPELKLRIFRLLDVRSVLSLSAVCRDLFTASNDPLMRFYLDRFNDTVRVDOTW 392
 QY 393 KELRKRIHOKKESPKGPFVWLPSSTHTTPEYENPPLHPPSPSSRLPGIIGEXYQRP 452
 DB 393 KELRKRIHOKKESPKGPFVWLPSSTHTTPEYENPPLHPPSPSSRLPGIIGEXYQRP 452
 QY 453 TLPYVGDPISSLLIPGEPHSPQPLRPREDPVGLPGPNPLFGRGGPNDRPFPSRS 512
 DB 453 TLPYVGDPISSLLIPGEPHSPQPLRPREDPVGLPGPNPLFGRGGPNDRPFPSRS 512
 QY 513 RPTGRLSEFM 522
 DB 513 RPTGRLSEFM 522
 RESULT 7
 AAU32109 standard; protein; 607 AA.
 XX
 AC AAU32109;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #2600.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US008656.
 XX
 PR 18-APR-2000; 2000US-00552929.
 XX
 PR 26-JAN-2001; 2001US-00770160.
 XX
 PA (HRSB-) HRSB INC.
 XX

PI Tang YT, Liu C, Drenth RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 XX vaccination, testing and therapy.
 PS Claim 20; Page 556; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration, immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemia.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 SQ Sequence 607 AA;
 Query Match 67.8%; Score 354; DB 4; Length 607;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 SLICTWGYSSNTRFTITLNYKDPPLTGDEETLASGYISGDLICILLODDIPAPNIPSSD 92
 DB 66 SLICTWGYSSNTRFTITLNYKDPPLTGDEETLASGYISGDLICILLODDIPAPNIPSSD 127
 QY 93 SEHSLSQNNNEPISLATSSNOTSMODEPSPDSFOGQAQSGVWDDSMIGSQNFABESIQ 152
 DB 128 SEHSLSQNNNEPISLATSSNOTSMODEPSPDSFOGQAQSGVWDDSMIGSQNFABESIQ 187
 QY 153 DNAMAEGTGFPSEPMKCSSEVGEQVPHSETLYQSGADSDANDALIVLHLMLESGY 212
 DB 188 DNAMAEGTGFPSEPMKCSSEVGEQVPHSETLYQSGADSDANDALIVLHLMLESGY 247
 QY 213 IPQGTAKALSMPEKMKLSGYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
 DB 248 IPQGTAKALSMPEKMKLSGYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 307
 QY 273 SVKRLQLLPESFTCKEKLGENVANITYKDLQKLSLTFDOLVYPLAFTROALNLPVFG 332
 DB 308 SVKRLQLLPESFTCKEKLGENVANITYKDLQKLSLTFDOLVYPLAFTROALNLPVFG 367
 QY 333 VVLPELKLRIFRLLDVRSVLSLSAVCRDLFTASNDPLMRFYLDRFNDTVR 386
 DB 368 VVLPELKLRIFRLLDVRSVLSLSAVCRDLFTASNDPLMRFYLDRFNDTVR 421
 RESULT 8
 AAB35160 standard; protein; 443 AA.
 XX
 AC AAB35160;
 XX
 DT 09-APR-2001 (first entry)
 XX
 DE Human Skp1-associated F-box protein-1 SAF-1alpha SEQ ID NO: 8.
 XX
 KW Human; protein degradation; shah-mediated degradation protein; SMP;
 KW SCF-complex protein; SCP; shah-1alpha; shah-1 interacting protein; SIP;
 KW Skp1-associated F-box protein; SAF-1; SAF-2; SMD; cancer; cell division;
 KW Skp1-associated destruction-box protein; inflammatory disease.
 XX

DB 146 VVATIKNNIRSVKQLQLPESFICKKNGENVANIYDLOQLSLFPDQVYPLAF 205
 QY 320 TRQALNPDVGVGLVPLLEKLRIFRLLDVRSVLSAVCRDLFTASNDPLMRFLYLRD 379
 DB 206 TRQALNPDVGVGLVPLLEKLRIFRLLDVRSVLSAVCRDLFTASNDPLMRFLYLRD 265
 QY 380 FRDNTVRVQDPTDMKELVYRKHIQKESPKGR 410
 DB 266 FRDNTVRVQDPTDMKELVYRKHIQKESPKGR 296

RESULT 10
 ADJ68946
 ID ADJ68946 standard; protein; 221 AA.
 AC ADJ68946;
 DT 06-MAY-2004 (first entry)
 DE Human heat mitochondrial protein as a therapeutic target SeqID752.
 XX
 KW Mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; noctropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytosstatic.
 XX
 OS Homo sapiens.
 PN WO2003087768-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010870.
 XX
 PR 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 PI Ghosh SS, Fathy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
 PI Warnock DE;
 DR WPI; 2003-845369/78.
 XX
 PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function;
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 PS Claim 1; SEQ ID NO 752; 180bp; English.
 XX
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heat mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, noctropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytosstatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.

SEQ Sequence 221 AA;
 Query Match 44.3%; Score 221; DB 7; Length 221;
 Best Local Similarity 100.0%; Pred. No. 3,7e-222;
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 ENVANIYKLOQLSLFPDQVYPLAFTRQALNPDVGVGLVPLLEKLRIFRLLDVRS 351
 DB 1 ENVANIYKLOQLSLFPDQVYPLAFTRQALNPDVGVGLVPLLEKLRIFRLLDVRS 60
 QY 352 VLSAVCRDLFTASNDPLMRFLYLRDNTVRVQDPTDMKELVYRKHIQKESPKGRF 411
 DB 61 VLSAVCRDLFTASNDPLMRFLYLRDNTVRVQDPTDMKELVYRKHIQKESPKGRF 120
 QY 412 VMLPSSSTHTIPFYENPLHPRFPSSRLPPGIIGGYDQRPPLPYGDPISLLPGGET 471
 DB 121 VMLPSSSTHTIPFYENPLHPRFPSSRLPPGIIGGYDQRPPLPYGDPISLLPGGET 180
 QY 472 PQQFPPLRRPDVGVGLPQPNPILPGRGPPNDRFPFRSRGRPTDGRLSFM 522
 DB 181 PQQFPPLRRPDVGVGLPQPNPILPGRGPPNDRFPFRSRGRPTDGRLSFM 221

RESULT 11
 ADAS4155
 ID ADAS4155 standard; protein; 221 AA.
 AC ADAS4155;
 DT 20-NOV-2003 (first entry)
 DE Human protein, SEQ ID 1723.
 XX
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Noctropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.
 XX
 OS Homo sapiens.
 PN EP1293569-A2.
 XX
 PD 19-MAR-2003.
 XX
 PF 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 DR WPI; 2003-395539/38.
 DR N-PSDB; ADA52516.
 XX
 PT New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 XX
 PS Claim 14; SEQ ID NO 1723; 205bp; English.
 XX
 CC The present invention relates to novel human secretory or membrane
 CC proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS2433-
 CC ADAS5072). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.

Query Match 38.3%; Score 200; DB 6; Length 221;

Best Local Similarity 100.0%; Pred. No. 3.8e-191; Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDVGVLVPLELKLRIFFRLDVRSVLSAVCRDLFTASNDPLMRELYLRDPRD 382
 Db 22 ALNLPDVGVLVPLELKLRIFFRLDVRSVLSAVCRDLFTASNDPLMRELYLRDPRD 81
 QY 363 NTVRVQDTWKELRKRHIOKESPKGRFVWMLPSSSTHTIPFYNPPLHPRPFPSSRLPPG 442
 Db 82 NTVRVQDTWKELRKRHIOKESPKGRFVWMLPSSSTHTIPFYNPPLHPRPFPSSRLPPG 141
 QY 443 IIGGEYDQRPFTLPYVGDPISSLLPGGETPSQFPPLRPFPDVGPLPGPNPLPGRCGN 502
 Db 142 IIGGEYDQRPFTLPYVGDPISSLLPGGETPSQFPPLRPFPDVGPLPGPNPLPGRCGN 201
 QY 503 DRFPFRPSRGRPTDGRLSFM 522
 Db 202 DRFPFRPSRGRPTDGRLSFM 221

RESULT 12

ID ABB90109 standard; protein; 462 AA.

AC ABB90109;
 XX
 XX 24-MAY-2002 (first entry)
 DT
 XX

DE Human polypeptide SEQ ID NO 2485.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX WO200190304-A2.

XX 29-NOV-2001.

XX 18-MAY-2001; 2001WO-US016450.

XX 19-MAY-2000; 2000US-0205515P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-122018/16.

XX N-PSDB; ABL90518.

PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.

PS Claim 11; SEQ ID NO 2485; 2061pp + Sequence Listing; English.

XX The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABB90040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune hemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)

CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: the sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 462 AA;

Query Match 38.3%; Score 200; DB 5; Length 462;
 Best Local Similarity 100.0%; Pred. No. 7.3e-191; Indels 0; Gaps 0;
 Matches 200; Conservative 0; Mismatches 0;

QY 323 ALNLPDVGVLVPLELKLRIFFRLDVRSVLSAVCRDLFTASNDPLMRELYLRDPRD 382
 Db 263 ALNLPDVGVLVPLELKLRIFFRLDVRSVLSAVCRDLFTASNDPLMRELYLRDPRD 322
 QY 383 NTVRVQDTWKELRKRHIOKESPKGRFVWMLPSSSTHTIPFYNPPLHPRPFPSSRLPPG 442
 Db 323 NTVRVQDTWKELRKRHIOKESPKGRFVWMLPSSSTHTIPFYNPPLHPRPFPSSRLPPG 382
 QY 443 IIGGEYDQRPFTLPYVGDPISSLLPGGETPSQFPPLRPFPDVGPLPGPNPLPGRCGN 502
 Db 383 IIGGEYDQRPFTLPYVGDPISSLLPGGETPSQFPPLRPFPDVGPLPGPNPLPGRCGN 442
 QY 503 DRFPFRPSRGRPTDGRLSFM 522
 Db 443 DRFPFRPSRGRPTDGRLSFM 462

RESULT 13

ID ADA57586 standard; protein; 462 AA.

AC ADA57586;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX

DE Human secreted protein #566.

XX immunosuppressive; anti-inflammatory; antiallergic;
 KW cytosstatic; cerebroprotective; neuroprotective; nootropic;
 KW cardiovascular; antiarteriosclerotic; gene therapy;
 KW human secreted protein; immune disorder; inflammation;
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
 KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.

XX WO2002102994-A2.

XX 27-DEC-2002.

XX 19-MAR-2002; 2002WO-US008278.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-167512/16.

XX N-PSDB; ADA56693.

PT New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.
 PS Claim 13; SEQ ID NO 1779; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 462 AA;

Query Match 38.3%; Score 200; DB 6; Length 462;

Best Local Similarity 100.0%; Pred. NO. 7.3e-191; Indels 0; Gaps 0;

Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDVGVLVPLELKLRIFFLLDVRSVLSAVCRDFTASNDPLMRFYLRDFRD 382
DB 263 ALNLPDVGVLVPLELKLRIFFLLDVRSVLSAVCRDFTASNDPLMRFYLRDFRD 322
QY 383 NTAVVQOTDWEKELRKKHIOKESPKGRFWLLPSSHTTTPFYNPPLHPPFPSSRLPPG 442
DB 323 NTAVVQOTDWEKELRKKHIOKESPKGRFWLLPSSHTTTPFYNPPLHPPFPSSRLPPG 382
QY 443 IIGGEYDORPFLPYVGDPISSILIPGPGTSPQFPPLRFRDPVGPLPGPNILPGRGPN 502
DB 383 IIGGEYDORPFLPYVGDPISSILIPGPGTSPQFPPLRFRDPVGPLPGPNILPGRGPN 442
QY 503 DRFPFRSGRGRPTDGRLSFM 522
DB 443 DRFPFRSGRGRPTDGRLSFM 462

RESULT 14

ADA41482
ID ADA41482 standard; protein, 462 AA.

XX ADA41482;

XX 20-NOV-2003 (first entry)

XX Human secreted protein.

XX Human, secreted protein; cancer; hyperproliferative disorder;
XX rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
XX anaemia; allergic reaction; asthma; cardiovascular disorder;
XX wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
XX antiviral; antileptotic; hepatotropic; antidiabetic; antiinflammatory;
XX vulnery; cardiant; gene therapy.

XX Homo sapiens.
XX OS
XX

PN WO2002102993-A2.
XX
XX 27-DEC-2002.
XX
XX 19-MAR-2002; 2002MO-US008123.
XX
XX 21-MAR-2001; 2001US-0277340P.
XX 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0331287P.
XX (HUMA-1) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPL, 2003-175238/17.
XX
XX New human secreted proteins and nucleic acid molecules, useful for
XX preparing a diagnostic or pharmaceutical composition for diagnosing,
XX preventing or treating cancer or other hyperproliferative disorder,
XX asthma, allergies or AIDS.

Claim 1; SEQ ID NO 1865; 3205pp; English.

XX The invention relates to novel genes ADA39629-ADA40565 and proteins
XX ADA40566-ADA41501 for human secreted proteins, useful for preventing,
XX treating or ameliorating medical conditions e.g. by protein or gene
XX therapy. The polypeptides, nucleic acid molecules, antibodies or their
XX fragments, and agonists or antagonists that bind to the polypeptide are
XX useful for preparing a diagnostic or pharmaceutical composition for
XX diagnosing or treating cancer or other hyperproliferative disorder. The
XX polypeptides and nucleic acid molecules are also useful for detecting,
XX preventing, diagnosing, prognosticating, treating or ameliorating cancer
XX or other hyperproliferative disorders including neoplasms, autoimmune
XX disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
XX erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
XX anaemia), haematopoietic or hematological disorders (e.g. anaemia,
XX thrombocytopenia), allergic reactions including asthma or eczema,
XX inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
XX bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
XX Alzheimer's disease or Parkinson's disease), cardiovascular disorders
XX (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
XX fungal or viral infections including HIV/AIDS), or wound healing and
XX disorders of epithelial cell proliferation. The nucleic acids are also
XX useful for chromosome identification, radiation hybrid mapping or long-
XX range restriction mapping, as molecular weight markers, or as
XX hybridization or diagnostic probes. The polypeptides and antibodies are
XX useful for providing immunohistochemistry assays. Note: The sequence data for
XX of the tissues immunohistochemistry assays. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 462 AA;

Query Match 38.3%; Score 200; DB 6; Length 462;

Best Local Similarity 100.0%; Pred. NO. 7.3e-191; Indels 0; Gaps 0;

Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDVGVLVPLELKLRIFFLLDVRSVLSAVCRDFTASNDPLMRFYLRDFRD 382
DB 263 ALNLPDVGVLVPLELKLRIFFLLDVRSVLSAVCRDFTASNDPLMRFYLRDFRD 322
QY 383 NTAVVQOTDWEKELRKKHIOKESPKGRFWLLPSSHTTTPFYNPPLHPPFPSSRLPPG 442
DB 323 NTAVVQOTDWEKELRKKHIOKESPKGRFWLLPSSHTTTPFYNPPLHPPFPSSRLPPG 382
QY 443 IIGGEYDORPFLPYVGDPISSILIPGPGTSPQFPPLRFRDPVGPLPGPNILPGRGPN 502
DB 383 IIGGEYDORPFLPYVGDPISSILIPGPGTSPQFPPLRFRDPVGPLPGPNILPGRGPN 442
QY 503 DRFPFRSGRGRPTDGRLSFM 522
DB 443 DRFPFRSGRGRPTDGRLSFM 462

RESULT 15

ABR48139
ID ABR48139 standard; protein; 462 AA.
XX
AC ABR48139;
XX
DI 12-JUN-2003 (first entry)
XX
DE Human secreted protein, SEQ ID 1030.
XX
KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
KW vulnery; antiinflammatory; nootropic; neuroprotective;
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.
XX
OS Homo sapiens.
XX
PN MO200295010-A2.
XX
PD 28-NOV-2002.
XX
PF 19-MAR-2002; 2002WC-US009785.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR MPI, 2003-129429/12.
XX
PT Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
PT disorders such as arrhythmia.
XX
PS Claim 13; SEQ ID NO 1030; 1881pp; English.
XX
CC The present invention relates to novel human secreted proteins (ABR47633-
CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
CC and their coding sequences are useful for the preparation of a diagnostic
CC or pharmaceutical composition for diagnosing or treating a cardiovascular
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders,
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal, regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism. Note: The sequence data for this patent was published in
CC electronic format and is available from WIPO at
CC ftp.wipo.int/pub/published_pot_sequences
XX
SQ Sequence 462 AA;

Query Match 38.3%; Score 200; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 7.3e-191;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 323 ALNLDPVFGVIVPLEIKRIIFRLLDVRSVLSASACRDIFTSNDPLMRPLYLARDPFD 382
DB 263 ALNLDPVFGVIVPLEIKRIIFRLLDVRSVLSASACRDIFTSNDPLMRPLYLARDPFD 322

QY 383 NTVRVQDTDWKELYRKRHIORKESPKGRFVMLPSSTHTIIPYPNLHPRPSPSSRLPPG 442
DB 323 NTVRVQDTDWKELYRKRHIORKESPKGRFVMLPSSTHTIIPYPNLHPRPSPSSRLPPG 382
QY 443 IIGGEYQRPPTLPYVGPISLLPGGETPSCRPPLRPREDPVGPIRGPPRIIPGRGGPN 502
DB 383 IIGGEYQRPPTLPYVGPISLLPGGETPSCRPPLRPREDPVGPIRGPPRIIPGRGGPN 442
QY 503 DRPFPRSPRGRPTDGRLSFM 522
DB 443 DRPFPRSPRGRPTDGRLSFM 462

RESULT 16

ADC74596
ID ADC74596 standard; protein; 462 AA.
XX
AC ADC74596;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted protein - SEQ ID 1229.
XX
KW antianaemic; antirheumatic; antiarrhythmic; antiinflammatory; antithyroid;
KW antidiabetic; immunosuppressive; dermatological; nephrotoxic;
KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
KW fungicide; antiparasitic; antiarteriosclerotic; vulnery; cytostatic;
KW haemopoietic; haematologic; anaemia; autoimmune disorder;
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
KW human.
XX
OS Homo sapiens.
XX
PN MO2003038063-A2.
XX
PD 08-MAY-2003.
XX
PF 19-MAR-2002; 2002WC-US008277.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR MPI, 2003-430516/40.
XX
PT New human secreted polypeptide for diagnosing, preventing or treating
PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
PT atherosclerosis).
XX
PS Claim 16; SEQ ID NO 1229; 2272pp; English.
XX
CC The invention relates to a novel human secreted polypeptide comprising a
CC defined sequence given in the specification. The polypeptide, nucleic
CC acid molecule, antibody, agonist or antagonist of the invention may be
CC useful for preparing a composition for diagnosing or treating a
CC haemopoietic or haematologic disorder such as anaemia, autoimmune
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC diabetes, systemic lupus erythematosus or glomerulonephritis,
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC disease, wounds and hyperproliferative disorders including
CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
CC parasitic infections. The polypeptide may also be used during gene
CC therapy procedures and for identifying a binding partner by contacting

CC the polypeptide with a binding partner and determining whether the
CC binding partner increases or decreases the activity of the polypeptide.
CC The current sequence is that of the human secreted protein of the
CC invention.
XX
SQ Sequence 462 AA;
Query Match 38 3%; Score 200; DB 7; Length 462;
Best Local Similarity 100.0%; Pred. No. 7.3e-191;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 323 ALNLPDVGVLVPLELKLRIPLLDVRSVLSAVCRDLFTASNDPLLMRPILYLRDPD 382
DB 263 ALNLPDVGVLVPLELKLRIPLLDVRSVLSAVCRDLFTASNDPLLMRPILYLRDPD 322
QY 383 NTVRVQDTWKELRYKRNHIOKESPKGRFVMLLPSSHTITPFYFNPLHRRPPSSSLPPG 442
DB 323 NTVRVQDTWKELRYKRNHIOKESPKGRFVMLLPSSHTITPFYFNPLHRRPPSSSLPPG 382
QY 443 IIGGEYQQRFTLPYVGPISLLPGQETPSQFPPLRPREDPVGPPLPGEPNLPFGSGGN 502
DB 383 IIGGEYQQRFTLPYVGPISLLPGQETPSQFPPLRPREDPVGPPLPGEPNLPFGSGGN 442
QY 503 DRPFPRSGRPFDDGRLSFM 522
DB 443 DRPFPRSGRPFDDGRLSFM 462
RESULT 17
ABG18510
ID ABG18510 standard; protein; 549 AA.
XX
AC ABG18510;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #18501.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US000631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS82697.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 48869; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pcr_sequences
XX
SQ Sequence 549 AA;
Query Match 25.7%; Score 134; DB 4; Length 549;
Best Local Similarity 100.0%; Pred. No. 9.6e-125;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 SLCTWGYSSNTRTITLNYKDPITGDETLASGYISGLICLIODDIPAPYIPSTSD 92
DB 34 SLCTWGYSSNTRTITLNYKDPITGDETLASGYISGLICLIODDIPAPYIPSTSD 93
QY 93 SEHSLQNNQEPISLATSSNQTSMQDEQPSDFQGOAAQSGVWDDSMIGSPQNFEEISIQ 152
DB 94 SEHSLQNNQEPISLATSSNQTSMQDEQPSDFQGOAAQSGVWDDSMIGSPQNFEEISIQ 153
QY 153 DNAMABEGTGFYPS 166
DB 154 DNAMABEGTGFYPS 167
RESULT 18
ADA57587
ID ADA57587 standard; protein; 174 AA.
XX
AC ADA57587;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein #566.
XX
KW Immunosuppressive; antiinflammatory; antiaslthmatic; antiallergic;
KW cytosstatic; cerebroprotective; neuroprotective; nocotropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.
XX
OS Homo sapiens.
XX
PN W02002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
XX
PR 19-JUN-2001; 2001US-0306171P.
XX
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI: 2003-167512/16.
DR N-PSDB; ADA56694.
XX

RESULT 20
ABR48140
ID ABR48140 standard; protein; 174 AA.
XX
XX
AC ABR48140;
XX
XX
DT 12-JUN-2003 (first entry)
XX
DE Human secreted protein, SEQ ID 1031.
XX
XX
KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cyostatic;
KW vulnerary; antiinflammatory; nootropic; neuroprotective;
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200295010-A2.
XX
XX
PD 28-NOV-2002.
XX
XX
PF 19-MAR-2002; 2002MO-US009785.
XX
XX
PR 21-MAR-2001; 2001US-0277340P.
XX
PR 19-JUL-2001; 2001US-0306171P.
XX
PR 13-NOV-2001; 2001US-0331287P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Ruben SM;
XX
XX
DR WPI; 2003-129429/12.
XX
XX
PT Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
PT disorders such as arrhythmia.
XX
XX
PS Claim 13; SEQ ID NO 1031; 1881bp; English.
XX
XX
CC The present invention relates to novel human secreted proteins (ABR47633-
CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
CC and their coding sequences are useful for the preparation of a diagnostic
CC or pharmaceutical composition for diagnosing or treating a cardiovascular
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders,
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism. Note: The sequence data for this patent was published in
CC electronic format and is available from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 174 AA;
XX
XX
Query Match 24.5%; Score 128; DB 6; Length 174;
Best Local Similarity 100.0%; Pred. No. 3,5e-119;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
OY LYRKRIORKEPSPGRFVLLPSTHTIPYPNLHPRPSPSSRLPGITIGGYDORPTL 454
DB 47 LYRKRIORKEPSPGRFVLLPSTHTIPYPNLHPRPSPSSRLPGITIGGYDORPTL 106
OY 455 PYVGDPISSLIPGGETPSPFPPLRPFPDVPGLPGNPILPGRGPNDRFPFRSGRP 514

DB 107 PYVGDPISSLIPGGETPSPFPPLRPFPDVPGLPGNPILPGRGPNDRFPFRSGRP 166
OY 515 TDGRLSEFM 522
DB 167 TDGRLSEFM 174
RESULT 21
ADC74597
ID ADC74597 standard; protein; 174 AA.
XX
XX
AC ADC74597;
XX
XX
DT 01-JAN-2004 (first entry)
XX
XX
DE Human secreted protein - SEQ ID 1230.
XX
XX
XX
KW antihaemic; antithaemic; antiarthritic; antiinflammatory; antithyroid;
KW antidiabetic; immunosuppressive; dermatological; nephrotropic;
KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cyostatic;
KW haemopoietic; haematologic; anaemia; autoimmune disorder;
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
KW human.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003038063-A2.
XX
XX
PD 08-MAY-2003.
XX
XX
PF 19-MAR-2002; 2002MO-US008277.
XX
XX
PR 21-MAR-2001; 2001US-0277340P.
XX
PR 19-JUL-2001; 2001US-0306171P.
XX
PR 13-NOV-2001; 2001US-0331287P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Ruben SM;
XX
XX
DR WPI; 2003-430516/40.
XX
XX
PT N-PSDB; ADC73982.
XX
XX
PT New human secreted polypeptide for diagnosing, preventing or treating
PT haematopoietic or hematologic disorders (e.g. anemia), autoimmune
PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
PT atherosclerosis).
XX
XX
PS Claim 16; SEQ ID NO 1230; 2272bp; English.
XX
XX
CC The invention relates to a novel human secreted polypeptide comprising a
CC defined sequence given in the specification. The polypeptide, nucleic
CC acid molecule, antibody, agonist or antagonist of the invention may be
CC useful for preparing a composition for diagnosing or treating a
CC haemopoietic or haematologic disorder such as anaemia, autoimmune
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC diabetes, systemic lupus erythematosus or glomerulonephritis,
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC disease, wounds and hyperproliferative disorders including
CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
CC parasitic infections. The polypeptide may also be used during gene
CC therapy procedures and for identifying a binding partner by contacting
CC the polypeptide with a binding partner and determining whether the
CC binding partner increases or decreases the activity of the polypeptide.
CC The current sequence is that of the human secreted protein of the
XX
XX
SQ Sequence 174 AA;
XX

Query Match 24.5%; Score 128; DB 7; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.5e-119; Mismatches 0; Indels 0; Gaps 0;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 LYKRHIQKESPKGRFVMLPSSTHTIPFYPNLHPRPSSRLPPGIIGEXYDQPTL 454
 DB 47 LYKRHIQKESPKGRFVMLPSSTHTIPFYPNLHPRPSSRLPPGIIGEXYDQPTL 106

QY 455 PYVGDPISLLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSGRP 514
 DB 107 PYVGDPISLLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSGRP 166

QY 515 TDGRLSFM 522
 DB 167 TDGRLSFM 174

RESULT 22
 AAY41397
 ID AAY41397 standard; protein; 175 AA.
 AC AAY41397;
 XX
 DT 02-DEC-1999 (first entry)
 XX
 DE Human secreted protein encoded by gene 90 clone HUSXS50.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 PN WO9947540-A1.
 PD 23-SEP-1999.
 XX
 PF 18-MAR-1999; 99WO-US005804.
 XX
 PR 19-MAR-1998; 98US-0078563P.
 PR 19-MAR-1998; 98US-0078566P.
 PR 19-MAR-1998; 98US-0078573P.
 PR 19-MAR-1998; 98US-0078574P.
 PR 19-MAR-1998; 98US-0078576P.
 PR 19-MAR-1998; 98US-0078577P.
 PR 19-MAR-1998; 98US-0078578P.
 PR 19-MAR-1998; 98US-0078579P.
 PR 19-MAR-1998; 98US-0078581P.
 PR 01-APR-1998; 98US-0080312P.
 PR 01-APR-1998; 98US-0080313P.
 PR 01-APR-1998; 98US-0080314P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Fang P, Soppet DR;
 PI Wei Y, Andrews GA, Duan RD, Kyaw H, Ebner R, Lafleur DW, Olsen HS;
 PI Shi Y, Moore PA;
 XX
 DR MPI: 1999-562050/47.
 DR N-PSDB; AAZ24900.
 XX
 PT New isolated human genes, useful for diagnosis and treatment of e.g.
 PT cancers, neurological disorders, immune diseases, inflammation or blood
 PT disorders.
 XX
 PS Claim 11; Page 411; 484pp; English.
 XX

CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAZ24802) for increasing the stability of the fused protein
 CC as compared to the human protein only. The invention relates to 95 novel
 CC genes and their fragments (nucleic acid sequences: AAZ24811-224907; amino
 CC acid sequences AAY41308-Y41404) which are useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
 CC pathological conditions can be diagnosed by determining the amount of the
 CC new polypeptides in a sample or by determining the presence of mutations
 CC in the new polynucleotides. Specific uses are described for each of the
 CC 95 polynucleotides, based on which tissues they are most highly expressed
 CC in (see AAZ24811 for described uses)

QY 395 LYKRHIQKESPKGRFVMLPSSTHTIPFYPNLHPRPSSRLPPGIIGEXYDQPTL 454
 DB 47 LYKRHIQKESPKGRFVMLPSSTHTIPFYPNLHPRPSSRLPPGIIGEXYDQPTL 106

QY 455 PYVGDPISLLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSGRP 514
 DB 107 PYVGDPISLLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSGRP 166

QY 515 TDGRLSFM 522
 DB 167 TDGRLSFM 174

RESULT 23
 AAY83047
 ID AAY83047 standard; protein; 482 AA.
 XX
 AC AAY83047;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE F-box protein FBP-7.
 XX
 KW F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist;
 KW proliferative disorder; differentiative disorder; breast cancer;
 KW prostate cancer; ovarian cancer; cancer; small cell lung carcinoma;
 KW immune disorder; cardiovascular disorder; inflammatory disorder; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200012679-A1.
 PD 09-MAR-2000.
 XX
 PF 27-AUG-1999; 99WO-US019560.
 XX
 PR 28-AUG-1998; 98US-0098355P.
 PR 03-FEB-1999; 99US-0118568P.
 PR 15-MAR-1999; 99US-0124449P.
 XX
 PA (UYNY) UNIV NEW YORK STATE.
 PI Chaur DS, Pagano M, Latres E;
 PI
 XX
 DR MPI: 2000-256635/22.
 DR N-PSDB; AAZ93356.
 XX
 PT Novel nucleic acid for screening compounds useful for treating
 PT proliferative and differentiative disorders such as cancer and immune
 PT disorders comprises sequences encoding ubiquitin ligases.
 XX
 PS Claim 10; Fig 10a; 245pp; English.
 XX

CC Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases
CC with F-box motifs (F-box proteins) are useful for diagnosis of
CC proliferative and differentiated related disorders by measuring FBP gene
CC expression. Cells expressing such proteins or their fragments are useful
CC for screening compounds. The compounds are agonists or antagonists, which
CC are useful for treating a proliferative or differentiative disorder in a
CC mammal such as breast, ovarian and prostate cancer and small cell lung
CC carcinoma and also major opportunistic infections, immune disorders,
CC cardiovascular diseases and inflammatory disorders. FBP protein, analogs,
CC derivatives and their subsequences, anti-FBP antibodies are also useful
CC in diagnosis of the disorders
CC
SQ Sequence 482 AA;
Query Match 16.5%; Score 86; DB 3; Length 482;
Best Local Similarity 100.0%; Pred. No. 9.4e-77;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 242 LCEGSSATLTCVPLGNLIVNATLKINNEISVKRLQLPESFICKELGENVANIYKDL 301
DB 202 LCEGSSATLTCVPLGNLIVNATLKINNEISVKRLQLPESFICKELGENVANIYKDL 261
QY 302 QKLSRLFKDQLVYPLLAFTROALNLP 327
DB 262 QKLSRLFKDQLVYPLLAFTROALNLP 287
RESULT 24
AAO22452
ID AAO22452 standard; protein; 482 AA.
AC AAO22452;
XX
DT 11-OCT-2002 (first entry)
DE Human F-box protein FBP7 SEQ ID No 14.
XX
XX Cytostatic; immunomodulator; cardiac; antiinflammatory; antimicrobial;
XX proliferative; differentiative disorder; Skp2; F-box protein; cancer;
XX ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer;
XX small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP;
XX inflammatory disorder; lymphoma; major opportunistic infection;
XX certain cardiovascular disease; human.
XX
OS Homo sapiens.
XX
XX WO200255665-A2.
XX
XX 18-JUL-2002.
XX
XX 07-JAN-2002; 2002WO-US000311.
XX
XX 05-JAN-2001; 2001US-0260179P.
XX
XX (UNYNY) UNIV NEW YORK STATE.
XX
XX Pagano M;
XX
XX WPI: 2002-599665/64.
XX
XX N-PSDB; AAL41047.
XX
XX Screening compounds for treating proliferative disorders, e.g. breast
XX cancer or prostate cancer, infections or immune disorders, comprises
XX detecting a change in the activity of Skp2 with either p27 or Cks1.
XX
XX Disclosure; Fig 10; 246pp; English.
XX
XX The invention relates to screening compounds useful for the treatment of
XX proliferative or differentiative disorders comprising detecting a change
XX in the activity of Skp2 (F-box protein). The method is useful for
XX screening compounds for the treatment of proliferative or differentiative
XX disorders, particularly cancer. These compounds include small molecules,
XX or compounds or derivatives or analogues of the new ubiquitin ligases.

CC The compounds are useful for treating diseases such as cancer (e.g.
CC breast cancer, prostate cancer or ovarian cancer, lymphoma, small cell
CC lung carcinoma or parathyroid adenomas), major opportunistic infections,
CC immune disorders, certain cardiovascular diseases or inflammatory
CC disorders. This sequence represents an F-box protein (FBP) relating to
CC the invention
CC
SQ Sequence 482 AA;
Query Match 16.5%; Score 86; DB 5; Length 482;
Best Local Similarity 100.0%; Pred. No. 9.4e-77;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 242 LCEGSSATLTCVPLGNLIVNATLKINNEISVKRLQLPESFICKELGENVANIYKDL 301
DB 202 LCEGSSATLTCVPLGNLIVNATLKINNEISVKRLQLPESFICKELGENVANIYKDL 261
QY 302 QKLSRLFKDQLVYPLLAFTROALNLP 327
DB 262 QKLSRLFKDQLVYPLLAFTROALNLP 287
RESULT 25
ABO54274
ID ABO54274 standard; protein; 76 AA.
XX
XX ABO54274;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human genome derived single exon protein #508.
XX
XX Human; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
XX US2003134704-A1.
XX
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX (PENK/) PENN S G.
XX (RANK/) RANK D R.
XX (HANK/) HANZEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
XX
XX WPI: 2004-119264/12.
XX
XX Claim 45; SEQ ID NO 27908; 60pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridises under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon

CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC continuous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subexpression, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20030194704
 CC
 XX Sequence 76 AA;
 SQ
 Query Match 14.6%; Score 76; DB 8; Length 76;
 Best Local Similarity 100.0%; Pred. No. 1.9e-67;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 140 LGPSQNFSEASIQNMAHAEIGTGYPSPEPMICSPSYEGGVPHSLETLTYSADCSNDAL 139
 DB 1 LGPSQNFSEASIQNMAHAEIGTGYPSPEPMICSPSYEGGVPHSLETLTYSADCSNDAL 60
 QY 200 IVLHLMBSGYIPQ 215
 DB 61 IVLHLMBSGYIPQ 76
 RESULT 26
 AAU32107
 ID AAU32107 standard; protein, 94 AA.
 XX
 AC AAU32107;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #2598.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WC200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US008656.
 XX
 PR 18-APR-2000; 2000US-00552929.
 XX
 PR 26-JAN-2001; 2001US-00770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Dmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 XX vaccination, testing and therapy.
 XX
 PS Claim 20, Page 556, 765pp, English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukemias.
 CC AAU29510-AAU3304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 CC
 XX Sequence 94 AA;
 SQ
 Query Match 12.1%; Score 63; DB 4; Length 94;
 Best Local Similarity 100.0%; Pred. No. 2.3e-54;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 425 YENPLHPRFPSSRLPPGIGGEYDQRTLPYVGDPISSLIPGDETPSPPLRFRDP 484
 DB 11 YENPLHPRFPSSRLPPGIGGEYDQRTLPYVGDPISSLIPGDETPSPPLRFRDP 70
 QY 485 VGP 487
 DB 71 VGP 73
 RESULT 27
 AA87356
 ID AA87356 standard; protein, 113 AA.
 XX
 AC AA87356;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSP-133 SEQ ID NO:133.
 XX
 KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; chronic disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 PN WC200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US014484.
 XX
 PR 26-JUN-1998; 98US-0090762P.
 XX
 PR 31-JUL-1998; 98US-0094983P.
 XX
 PR 01-OCT-1998; 98US-0102686P.
 XX
 PR 11-DEC-1998; 98US-0112129P.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KT, Baughn MR;
 XX Akerblom IE, Au-Yang J, Yue H, Patterson C, Reddy R, Hillman JL;
 XX Bandman O;

DR WPI; 2000-160673/14.
DR N-PSDB; AA298241.
XX
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
PT disease.
XX
XX
PS Claim 1; Page 251; 327pp; English.

XX AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antiautismic activities, and can be
CC used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
CC or ribozyme therapeutics, for detecting related sequences or genetic
CC variations, and for chromosomal mapping. HSP are also used to raise
CC specific antibodies (Ab) and to screen for agonists and antagonists
CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP
CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
CC competitive drug screens, and for purification of HSP from natural
CC sources
XX
XX

XX Sequence 113 AA;

Query Match 11.3%; Score 59; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.7e-50;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 323 ALNPDVGVGLVPLPELKLRIFFLLDVRSVLSAVCRDLFTASNDPLMRFYLRDR 381
Db 22 ALNPDVGVGLVPLPELKLRIFFLLDVRSVLSAVCRDLFTASNDPLMRFYLRDR 80

RESULT 28

ABG06838
ID ABG06838 standard; protein; 225 AA.

XX AC ABG06838;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #6829.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US0008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.
DR N-PSDB; AA571025.

XX
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX

PS Claim 20; SEQ ID NO 37197; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABO0010-AB030377 represent novel human diagnostic
CC amino acid sequences. ABO0010-AB030377 represent novel human diagnostic
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

XX Sequence 225 AA;

Query Match 10.2%; Score 53; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 329 VGVGLVPLPELKLRIFFLLDVRSVLSAVCRDLFTASNDPLMRFYLRDR 381
Db 3 VGVGLVPLPELKLRIFFLLDVRSVLSAVCRDLFTASNDPLMRFYLRDR 55

RESULT 29

ABO59862
ID ABO59862 standard; protein; 47 AA.

XX AC ABO59862;

XX DT 29-JUL-2004 (first entry)

XX DE Human genome derived single exon protein #6096.

XX KW Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.

XX OS Homo sapiens.

XX PN US2003194704-A1.

XX PD 16-OCT-2003.

XX PF 03-APR-2002; 2002US-00029386.

XX PR 03-APR-2002; 2002US-00029386.

XX PA (PENN/) PENN S G.

XX PA (RANK/) RANK D R.

XX PA (HANZ/) HANZEL D K.

XX PI Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX
 PS Claim 45; SEQ ID NO 33496; 80pp; English.
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC a method of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20030194704
 CC
 XX
 SQ Sequence 47 AA:
 Query Match 9.0%; Score 47; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 1.3e-38;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 216 GTEAKALSMPEKWLKSGVYKLYQVHPLCEGSSATLTCVPLGNLIVV 262
 DB 1 GTEAKALSMPEKWLKSGVYKLYQVHPLCEGSSATLTCVPLGNLIVV 47
 RESULT 30
 AAY83054
 ID AAY83054 standard; peptide; 39 AA.
 XX
 AC AAY83054;
 XX
 DT 16-AUG-2000 (first entry)
 DE F-box motif of FBP-6.
 XX
 XX F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist;
 KM proliferative disorder; differentiative disorder; breast cancer;
 KM prostate cancer; ovarian cancer; cancer; small cell lung carcinoma;
 KM immune disorder; cardiovascular disorder; inflammatory disorder; human.
 XX Homo sapiens.
 OS
 XX
 PN WO200012679-A1.

XX
 PD 09-MAR-2000.
 XX
 PF 27-AUG-1999; 99WO-US019560.
 XX
 XX 28-AUG-1998; 98US-0098355P.
 PR 03-FEB-1999; 99US-0118568P.
 PR 15-MAR-1999; 99US-0124449P.
 XX
 PA (UNYV) UNIV NEW YORK STATE.
 PI Chiau DS, Pagano M, Latres E;
 XX
 DR WPI, 2000-256635/22.
 XX
 PT Novel nucleic acid for screening compounds useful for treating
 PT proliferative and differentiative disorders such as cancer and immune
 PT disorders comprises sequences encoding ubiquitin ligases.
 XX
 PS Disclosure, Page 197; 245pp; English.
 CC Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases
 CC with F-box motifs (F-box proteins) are useful for diagnosis of
 CC proliferative and differentiated related disorders by measuring FBP gene
 CC expression. Cells expressing such proteins or their fragments are useful
 CC for screening compounds. The compounds are agonists or antagonists, which
 CC are useful for treating a proliferative or differentiative disorder in a
 CC mammal such as breast, ovarian and prostate cancer and small cell lung
 CC carcinoma and also major opportunistic infections, immune disorders,
 CC cardiovascular diseases and inflammatory disorders. FBP protein, analogs,
 CC derivatives and their subsequences, anti-FBP antibodies are also useful
 CC in diagnosis of the disorders
 CC
 XX
 SQ Sequence 39 AA:
 Query Match 7.5%; Score 39; DB 3; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.1e-30;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 335 LPELKLRIPLDVRSLSSAVCRDFTASNDPLLR 373
 DB 1 LPELKLRIPLDVRSLSSAVCRDFTASNDPLLR 39
 RESULT 31
 ID AAO22459 standard; peptide; 39 AA.
 XX
 AC AAO22459;
 XX
 DT 11-OCT-2002 (first entry)
 DE Human F-box motif amino residues of FBP7 SEQ ID NO 21.
 XX
 XX Cytostatic; immunomodulator; cardiac; antiinflammatory; antimicrobial;
 KM proliferative; differentiative disorder; SgP2; F-box protein; cancer;
 KM ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer;
 KM small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP;
 KM inflammatory disorder; lymphoma; major opportunistic infection;
 XX certain cardiovascular disease; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200255665-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 07-JAN-2002; 2002MO-US000311.
 PR 05-JAN-2001; 2001US-0260179P.
 XX
 PA (UNYV) UNIV NEW YORK STATE.

XX
SQ Sequence 38 AA;

Query Match 7.3%; Score 38; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLELKRIFFRLDVRSVLSAVCRDLFTASNDPLIM 372
1 LPLELKRIFFRLDVRSVLSAVCRDLFTASNDPLIM 38

RESULT 34
AAB39652
ID AAB39652 standard; peptide; 38 AA.

AC AAB39652;

DT 18-DEC-2003 (first entry)

DE Human F-box protein, F18 (phl).

KW Human; F-box domain; E3 complex; ubiquitination; cell cycle regulator;
inflammatory disease.

OS Homo sapiens.

PN US6573094-B1.

PD 03-JUN-2003.

PF 16-OCT-1997; 97US-00951621.

PR 16-OCT-1997; 97US-00951621.

PA (BAYU) BAYLOR COLLEGE MEDICINE.

PI Harper JW, Ellledge SJ;

DR WPI; 2003-776006/73.
DR N-PSDB; AAD60321.

PT New isolated nucleic acid segment encoding a protein with at least one
functionally active F-box domain, useful for identifying related genes,
and for developing compounds for treating infectious or inflammatory
disease.

PS Example 6; Col 57-58; Opg; English.

CC The invention relates to an isolated nucleic acid segment comprising or
consisting essentially of a nucleic acid sequence encoding a protein
comprising at least one functionally active F-box domain sequence. The
polypeptide encoded by the nucleic acid segment is part of an E3 complex
involved in ubiquitination of cell cycle regulators and may be useful in
investigating mechanisms of infectious and inflammatory diseases and in
developing therapeutic agents for treating such diseases. The invention
is useful for detecting related polynucleotides encoding F-box proteins
CC and in the determination of the function of proteins such as elongin C,
CC Skp1-related protein, elongin B and elongin A. The present sequence is
CC human F-box protein
CC
XX

SQ Sequence 38 AA;

Query Match 7.3%; Score 38; DB 7; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLELKRIFFRLDVRSVLSAVCRDLFTASNDPLIM 372
1 LPLELKRIFFRLDVRSVLSAVCRDLFTASNDPLIM 38

RESULT 35

ABG18509
ID ABG18509 standard; protein; 53 AA.

AC ABG18509;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #18500.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.
DR N-PSDB; AAS82696.

PT New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 48668; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease, states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
XX

SQ Sequence 53 AA;

Query Match 6.1%; Score 32; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.5e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 491 PNPILPGRGENDRPPFRPSRGPRPTDGRLSFM 522
22 PNPILPGRGENDRPPFRPSRGPRPTDGRLSFM 53

RESULT 36
AAU32108
ID AAU32108 standard; protein; 53 AA.

```

XX AC AAU32108;
XX XX
XX DT 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #2599.
XX KM Human; vaccination; gene therapy; nutritional supplement;
XX KM stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KM immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS Homo sapiens.
XX PN WO200179449-A2.
XX PD 25-OCT-2001.
XX PF 16-APR-2001; 2001WO-US0008656.
XX PR 18-APR-2000; 2000US-00552929.
XX PR 26-JAN-2001; 2001US-00770160.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI, 2001-611725/70.
XX PT Nucleic acids encoding a range of human polypeptides; useful in genetic
XX PT vaccination, testing and therapy.
XX PS Claim 20; Page 556; 765pp; English.
XX CC The invention relates to novel human secreted polypeptides. The
XX CC polypeptides and antibodies to the polypeptides are useful for
XX CC determining the presence of or predisposition to a disease associated
XX CC with altered levels of polypeptide. The polypeptides are also useful for
XX CC identifying agents (agonists and antagonists) that bind to them. Cells
XX CC expressing the proteins are useful for identifying a therapeutic agent
XX CC for use in treatment of a pathology related to aberrant expression or
XX CC physiological interactions of the polypeptide. Vectors comprising the
XX CC nucleic acids encoding the polypeptides and cells genetically engineered
XX CC to express them are also useful for producing the proteins. The proteins
XX CC are useful in genetic vaccination, testing and therapy, and can be used
XX CC as nutritional supplements. They may be used to increase stem cell
XX CC proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon
XX CC and/or nerve tissue growth or regeneration; immune suppression and/or
XX CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX CC AAU29510-AAU3304 represent the amino acid sequences of novel human
XX CC secreted proteins of the invention
XX SQ
SQ Sequence 53 AA;
Query Match 6.1%; Score 32; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.5e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 491 PNPILPGRGGRNDPRFRPSRGRPTDGRLSFM 522
DB 22 PNPILPGRGGRNDPRFRPSRGRPTDGRLSFM 53

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XX KM cell cycle regulator; transcription regulator; DNA replication;
XX KM inflammatory response; infectious disease; protein degradation; cancer;
XX KM virus infection.
XX OS Mus sp.
XX PN WO9918989-A1.
XX PD 22-APR-1999.
XX PF 15-OCT-1998; 98WO-US021763.
XX PR 16-OCT-1997; 97US-00951621.
XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX PI Harper JW, Ellledge SJ;
XX PT WPI, 1999-277441/23.
XX DR N-PSDB; AAX35547.
XX PT New isolated F-box proteins and genes for development of therapeutics,
XX PT e.g. for cancer treatment.
XX PS Claim 4; Page 110; 170pp; English.
XX CC AAX35523-51 encode F-box proteins (AAV02249-77) which are involved in the
XX CC targeted ubiquitination of cellular proteins. The F-box proteins are
XX CC involved in targeted ubiquitination of cellular proteins, including cell
XX CC cycle regulators. The products and methods can be used for determining
XX CC the interaction of these proteins with other proteins, e.g. to identify
XX CC and/or investigate cell cycle regulators, transcription regulators,
XX CC proteins involved in DNA replication, and other cellular regulatory
XX CC proteins. They can be used in elucidating inflammatory response and
XX CC infectious disease processes involving protein degradation as well as
XX CC development of compounds that control (i.e. either enhance or retard)
XX CC protein degradation, as appropriate to ameliorate the effects of the
XX CC inflammatory response or disease process. They can be used for
XX CC identifying and developing compounds effective against cancers or virus
XX CC infection, e.g. immunodeficiency viruses such as HIV, feline
XX CC immunodeficiency virus, bovine immunodeficiency virus, and simian
XX CC immunodeficiency virus
XX SQ
SQ Sequence 38 AA;
Query Match 2.9%; Score 15; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 335 LPLEKLRIRFLDDV 349
DB 1 LPLEKLRIRFLDDV 15

```

```

RESULT 37
AAV02273
ID AAV02273 standard; protein; 38 AA.
XX
XX AAV02273;
XX
XX 08-JUN-1999 (first entry)
XX
XX A F-box protein sequence.
XX
XX F-box protein; targeted ubiquitination; cellular protein.
XX

```

```

RESULT 38
AAE08045
ID AAE08045 standard; peptide; 38 AA.
XX
XX AAE08045;
XX
XX 01-NOV-2001 (first entry)
XX
XX Mouse F-box protein, F18 phi.
XX
XX Mouse; nuclear factor-kappaB; NF-kB; regulatory factor; slimb protein;
XX KM targeted ubiquitination; F-box protein; F18 phi.
XX
XX Mus musculus.
XX
XX US6232081-B1.
XX
XX 15-MAY-2001.
XX

```

PF 15-OCT-1998; 98US-00172841.
 XX
 PR 16-OCT-1997; 97US-00951621.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Harper JW, Ellledge SJ, Winston JT;
 XX
 DR WPI; 2001-342771/36.
 DR N-PSDB; AAD14882.
 XX
 PT Detecting nuclear factor-kappaB regulatory factors, such as F-box
 PT proteins involved in targeted ubiquitination, by contacting the
 PT regulatory factors with slimb protein to form a complex and detecting the
 PT complex.
 XX
 PS Example 6; Fig 7; 69pp; English.
 XX
 CC The present invention relates to a method for detection of one or more
 CC nuclear factor (NF)-kappaB (KB) regulatory factors. The method comprises
 CC exposing a slimb protein to a sample suspected of containing one or more
 CC NF-kB regulatory factors, so that the slimb protein binds to one or more
 CC NF-kB regulatory factors to form a slimb/regulatory factor complex and
 CC detecting the slimb/regulatory factor complex. The method is useful for
 CC detecting NF-kB regulatory factors such as F-box proteins, IKKs, IKKs and
 CC agonists, antagonists and cofactors that interact with these factors. F-
 CC box proteins are involved in targeted ubiquitination of cellular
 CC proteins. The present sequence is mouse F-box protein, F18 Phi
 CC
 SQ Sequence 38 AA;
 QY
 Query Match 2.9%; Score 15; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 335 LPELKLRIFFRLDV 349
 1 LPELKLRIFFRLDV 15
 RESULT 39
 AAB39653
 ID AAB39653 standard; peptide; 38 AA.
 XX
 AC AAB39653;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Mouse F-box protein, F18 (phi).
 XX
 KW Mouse; F-Box domain; E3 complex; ubiquitination; cell cycle regulator;
 KW inflammatory disease.
 XX
 OS Homo sapiens.
 XX
 PN US6573094-B1.
 XX
 PD 03-JUN-2003.
 XX
 PF 16-OCT-1997; 97US-00951621.
 XX
 PR 16-OCT-1997; 97US-00951621.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Harper JW, Ellledge SJ;
 XX
 DR WPI; 2003-776006/73.
 DR N-PSDB; AAD60322.
 XX
 PT New isolated nucleic acid segment encoding a protein with at least one
 PT functionally active F-box domain, useful for identifying related genes,
 PT and for developing compounds for treating infectious or inflammatory

PT disease.
 XX
 PS Example 6; Col 57-58; Opp; English.
 XX
 CC The invention relates to an isolated nucleic acid segment comprising or
 CC consisting essentially of a nucleic acid sequence encoding a protein
 CC comprising at least one functionally active F-box domain sequence. The
 CC polypeptide encoded by the nucleic acid segment is part of an E3 complex
 CC involved in ubiquitination of cell cycle regulators and may be useful in
 CC investigating mechanisms of infectious and inflammatory diseases and in
 CC developing therapeutic agents for treating such diseases. The invention
 CC is useful for detecting related polynucleotides encoding F-box proteins
 CC and in the determination of the function of proteins such as elongin C,
 CC Skp1-related protein, elongin B and elongin A. The present sequence is
 CC mouse F-box protein
 CC
 SQ Sequence 38 AA;
 QY
 Query Match 2.9%; Score 15; DB 7; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 335 LPELKLRIFFRLDV 349
 1 LPELKLRIFFRLDV 15
 RESULT 40
 AAY41578
 ID AAY41578 standard; protein; 13 AA.
 XX
 AC AAY41578;
 XX
 DT 02-DEC-1999 (first entry)
 XX
 DE Fragment of human secreted protein encoded by gene 90.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 PN WO947540-A1.
 XX
 PD 23-SEP-1999.
 XX
 PF 18-MAR-1999; 99WO-US005804.
 XX
 PR 19-MAR-1998; 98US-0078563P.
 PR 19-MAR-1998; 98US-0078566P.
 PR 19-MAR-1998; 98US-0078573P.
 PR 19-MAR-1998; 98US-0078574P.
 PR 19-MAR-1998; 98US-0078576P.
 PR 19-MAR-1998; 98US-0078577P.
 PR 19-MAR-1998; 98US-0078578P.
 PR 19-MAR-1998; 98US-0078579P.
 PR 19-MAR-1998; 98US-0078581P.
 PR 19-MAR-1998; 98US-0078581P.
 PR 01-APR-1998; 98US-0080313P.
 PR 01-APR-1998; 98US-0080313P.
 PR 01-APR-1998; 98US-0080314P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR;
 PI Wei Y, Endress CA, Duan RD, Kyaw H, Ebner R, Lafleur DW, Olsen HS;
 PI Shi Y, Moore PA;
 XX

DR WPI; 1999-562050/47.

XX
XX New isolated human genes, useful for diagnosis and treatment of e.g.
PT cancers, neurological disorders, immune diseases, inflammation or blood
PT disorders.

XX
XX Disclosure; Page 167; 484pp; English.

XX
XX This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule detailed in the descriptor line. The gene
CC can be used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AA224802) for increasing the stability of
CC the fused protein as compared to the human protein only. The invention
CC relates to 95 novel genes and their fragments (nucleic acid sequences:
CC AA224811-224907; amino acid sequences AA41308-Y41404) which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. Also, pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 95 polynucleotides, based on
CC which tissues they are most highly expressed in (see AA224811 for
CC described uses)

XX
XX Sequence 13 AA;

SO Query Match 2.5%; Score 13; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 ROALNLPVFGIV 333
DB 1 ROALNLPVFGIV 13

RESULT 41
AAV41577
ID AAV41577 standard; protein; 13 AA.

XX
XX AAV41577;

DT 02-DEC-1999 (first entry)

XX
XX Fragment of human secreted protein encoded by gene 90.

XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KM diagnosis; disease; cancer; tumour; neurodegenerative disorder; leukaemia;
KM developmental abnormality; foetal deficiency; blood; allergy; renal;
KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KM inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX
XX Homo sapiens.

XX
XX WO9947540-A1.

XX
XX 23-SEP-1999.

PD 18-MAR-1999; 99WO-US005804.

XX
XX 19-MAR-1998; 98US-0078563P.

XX
XX 19-MAR-1998; 98US-0078566P.

XX
XX 19-MAR-1998; 98US-0078573P.

XX
XX 19-MAR-1998; 98US-0078574P.

XX
XX 19-MAR-1998; 98US-0078576P.

XX
XX 19-MAR-1998; 98US-0078577P.

XX
XX 19-MAR-1998; 98US-0078578P.

XX
XX 19-MAR-1998; 98US-0078579P.

XX
XX 19-MAR-1998; 98US-0078581P.

XX
XX 01-APR-1998; 98US-0080312P.

XX
XX 01-APR-1998; 98US-0080313P.

XX
XX 01-APR-1998; 98US-0080314P.

XX
XX (HUMA-) HUMAN GENOME SCI INC.

XX
XX Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR;
PI Wei Y, Endress GA, Duan RD, Kyaw H, Ebner R, Lafleur DW, Olsen HS;
PI Shi Y, Moore PA;

XX
XX WPI; 1999-562050/47.

XX
XX New isolated human genes, useful for diagnosis and treatment of e.g.
PT cancers, neurological disorders, immune diseases, inflammation or blood
PT disorders.

XX
XX Disclosure; Page 167; 484pp; English.

XX
XX This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule detailed in the descriptor line. The gene
CC can be used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AA224802) for increasing the stability of
CC the fused protein as compared to the human protein only. The invention
CC relates to 95 novel genes and their fragments (nucleic acid sequences:
CC AA224811-224907; amino acid sequences AA41308-Y41404) which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. Also, pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 95 polynucleotides, based on
CC which tissues they are most highly expressed in (see AA224811 for
CC described uses)

XX
XX Sequence 13 AA;

SO Query Match 2.5%; Score 13; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 FKDQVYPLAFT 320
DB 1 FKDQVYPLAFT 13

RESULT 42
AAM94240
ID AAM94240 standard; protein; 57 AA.

XX
XX AAM94240;

DT 21-NOV-2001 (first entry)

XX
XX Human reproductive system related antigen SEQ ID NO: 2898.

XX
XX Human; reproductive system related antigen; reproductive system disorder;
KM cancer; gene therapy.

XX
XX Homo sapiens.

XX
XX WO200155320-A2.

XX
XX 02-AUG-2001.

PD 17-JAN-2001; 2001WO-US001339.

XX
XX 31-JAN-2000; 2000US-0179065P.

XX
XX 04-FEB-2000; 2000US-0180628P.

XX
XX 24-FEB-2000; 2000US-0184664P.

XX
XX 02-MAR-2000; 2000US-0186350P.

XX
XX 16-MAR-2000; 2000US-0189874P.

XX
XX 17-MAR-2000; 2000US-0190076P.

XX
XX 18-APR-2000; 2000US-0198123P.

XX
XX 19-MAY-2000; 2000US-020515P.

XX
XX 07-JUN-2000; 2000US-0209467P.

XX
XX 28-JUN-2000; 2000US-0214886P.

XX
XX 30-JUN-2000; 2000US-0215135P.

Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 406 SPKGRFVM 413
Db 1 SPKGRFVM 8

RESULT 43

ABO55854
ID ABO55854 standard; protein; 63 AA.
XX
AC ABO55854;
XX
DT 29-JUN-2004 (first entry)
XX
DE Human genome derived single exon protein #2088.
XX
KW Human; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PF 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
DR WPI; 2004-119264/12.
XX
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.

Claim 45; SEQ ID NO 29488; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene
expression, comprising any of the 27,400 fully defined nucleotide
sequences in the specification, or their complements or fragments, and
encoding at least 8 amino acids of any of the 6888 amino acid sequences
fully defined in the specification. The probe is a single exon probe that
hybridizes under high stringency conditions to a nucleic acid molecule
expressed in human cells or tissues. Also included are a spatially-
addressable set of single exon nucleic acid probes for measuring human
gene expression (comprising a plurality of single exon nucleic acid
probes cited above, where each of the plurality of probes is separately
and addressably isolatable or amplifiable from the plurality), a single
exon microarray for measuring human gene expression, a method of
measuring human gene expression, a vector comprising the single exon
probe cited above, an ORF-encoded peptide comprising at least 8
contiguous amino acids of any of the above-mentioned amino acid
sequences (optionally with conservative amino acid substitutions), an
isolated antibody that binds specifically to a peptide cited above,
a method of selling and/or licensing single exon probes or microarrays to
a customer desiring to measure gene expression, a method of providing
human gene expression data by subscription, and a computer-readable
storage medium which contains a database having a plurality of records
(each record including data on the expression of a single exon probe
cited above). The probe, methods and apparatus are useful in gene
expression analysis. The probes may be used as tools for surveying
tissues to detect the presence of expressed messages that contain their
specific exon, or in constructing genome-derived single exon microarrays.
In addition, the probes are used in identifying and characterizing

CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX

Seq Sequence 63 AA;

Query Match 1.5%; Score 8; DB 8; Length 63;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 350 RSVLSLSA 357
Db 32 RSVLSLSA 39

RESULT 44

ABP10900
ID ABP10900 standard; protein; 92 AA.
XX
AC ABP10900;
XX
DT 25-JUN-2002 (first entry)
XX
DE Human ORFX protein sequence SEQ ID NO:21782.
XX

KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumor; hemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.

OS Homo sapiens.

PN WO200192523-A2.

PD 06-DEC-2001.

PF 29-MAY-2001; 2001WO-US010836.

PR 30-MAY-2000; 2000US-0206132P.

PR 29-AUG-2000; 2000US-0228716P.

XX (CURA-) CURAGEN CORP.

XX Shinketsu RA, Leach MD;

XX WPI; 2002-106308/14.

XX N-PSDB; ABN26652.

XX PT

XX Novel human polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cardiovascular disease, neurodegenerative,
XX hyperproliferative disorders and autoimmune disorders.

XX Disclosure; SEQ ID NO 21782; 1037pp; English.

XX The present invention describes substantially purified human proteins
XX (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
XX in the specification). ABN15762 to ABN27252 encode the human ORFX
XX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
XX treating or preventing a pathology associated with an ORFX-associated
XX disorder in humans, and in the manufacture of a medicament for treating a
XX syndrome associated with ORFX-associated disorder. ORFX polynucleotide
XX sequences can be used in gene therapy. ORFX sequences can be used in the
XX treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
XX psoriasis, benign tumors, keloid, degenerative disorders, hemorrhage,

CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORF proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 92 AA;

Query Match 1.5%; Score 8; DB 5; Length 92;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 471 TPSEQPPL 478
 |||||
 72 TPSEQPPL 79

RESULT 45
 AAU55117
 ID AAU55117 standard; protein; 183 AA.

AC AAU55117;

XX 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #16013.

XX SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
 XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA,
 XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 XX dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US012865.

XX 21-APR-2000; 2000US-0199047P.

XX 02-JUN-2000; 2000US-0208841P.

XX 07-JUL-2000; 2000US-0216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI: 2001-616774/71.

XX N-PSDB; AAS59568.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.

XX Example 1; SEQ ID NO 16312; 1069pp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 183 AA;

Query Match 1.5%; Score 8; DB 4; Length 183;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 VPETEPPL 23
 |||||
 137 VPETEPPL 144

RESULT 46
 ABMS1636
 ID ABMS1636 standard; protein; 183 AA.

AC ABMS1636;

XX 20-OCT-2003 (first entry)

XX Propionibacterium acnes predicted ORF-encoded polypeptide #16312.

XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 XX immunostimulant; immune response; vaccine.

XX Propionibacterium acnes.

XX WO2003033515-A1.

XX 24-APR-2003.

XX 11-OCT-2002; 2002WO-US032727.

XX 15-OCT-2001; 2001US-00978825.

XX (CORI-) CORIXA CORP.

XX Mitcham JL, Skeiky YAM, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Valliave-Douglass J;

XX WPI: 2003-381789/36.

XX N-PSDB; ACF64497.

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.

XX Example 1; SEQ ID NO 16312; 1481pp; English.

CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared

via this method; a vaccine composition (comprising P. acnes polypeptides, CC polynucleotides, antibodies, fusion proteins, T cell populations, or CC antigen-presenting cells that express the polypeptide); a method and kit CC for detecting or determining the presence or absence of P. acnes in a CC patient; and a method for inhibiting the development of P. acnes in a CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion CC proteins, T cell populations or antigen-presenting cells that express the CC polypeptides are useful for diagnosing, preventing or treating acne CC vulgaris, or for stimulating an immune response specific for a P. acnes CC protein. The polynucleotides can also be used as probes or primers for CC nucleic acid hybridisation. The vaccine composition is useful for the CC stimulation of an immune response against P. acnes, or for treating acne, CC and the kit is useful for performing a diagnostic assay. The present CC sequence represents a polypeptide predicted to be encoded by an ORF (open CC reading frame) contained within the P. acnes polynucleotides of the CC invention. Note: The sequence data for this patent did not form part of CC the printed specification, but was obtained in electronic format directly CC from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences) CC

SQ Sequence 183 AA;

Query Match 1.5%; Score 8; DB 6; Length 183;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 VPETPEPTL 23
|||
DB 137 VPETPEPTL 144

RESULT 47

AAG32036 AAG32036 standard; protein; 572 AA.

AC AAG32036;

DI 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 38575.

XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000BP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130443P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-01310891P.

PR 30-APR-1999; 99US-0131449P.

PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 22-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 02-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143342P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.

PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145961P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147182P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150864P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151068P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153078P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0156589P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157533P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159333P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.

PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 26-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161932P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 1.5%; Score 8; DB 3; Length 572;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 DICTILQ 79
Db 96 DICTILQ 103

RESULT 48
AAG66450
ID AAG66450 standard; protein; 628 AA.
XX
AC AAG66450;
XX
DT 16-NOV-2001 (first entry)
XX
DE Murine beta-netrin.
XX
XX
KM Vulture; beta-netrin; cytostatic; Neurotrophic; Neuroprotective; Vasotrophic;
KM Vulture; gene therapy; neurite growth; neurite guidance; renal cancer;
KM neurite stability; cell proliferation; angiogenesis; Alzheimer's;
KM muscular development; muscular innervation; tumour; ovarian cancer;
KM neurological disorder; cardiovascular disorder; ischaemia.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 31 /note="Encoded by GAC"
FT Misc-difference 132.1134 /note="Encoded by ATG GTG TTC"
FT Misc-difference 227 /note="Encoded by ATG GTG TTC"
FT Misc-difference 227 /note="Encoded by CCG"
FT Misc-difference 249 /note="Encoded by ATG"
FT Misc-difference 341 /note="Encoded by TCT"
FT Misc-difference 558 /note="Encoded by AAC"
XX
PN WO200164837-A2.
XX
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006413.
XX
XX 29-FEB-2000; 2000US-0185811P.
PR 01-SEP-2000; 2000US-0229893P.
XX
PA (SEHO) GEN HOSPITAL CORP.
XX
XX Burgess R, Brunken W, Koch M, Hunter D, Olson P;
PI WPI; 2001-550173/61.
DR N-PSDB; AAH75956.
XX
PT Novel beta-netrin polypeptides, polynucleotides useful in neurite
PT outgrowth, stability, modulating angiogenesis, cell proliferation and for

PT treating and preventing cancer, neurological and cardiovascular disorders.

XX

PS Claim 5; Fig 3; 140pp; English.

XX

CC The present sequence is the protein sequence for murine beta-netrin. Beta-netrin is useful in neurite growth, guidance and/or stability. Beta-netrin is also useful in cell proliferation, development of the vascular system, angiogenesis, muscular development or innervation. Beta-netrin inhibits tumour growth and angiogenesis in tumours therefore, beta-netrin is useful for treating ovarian and renal cancer. Also, beta-netrin is useful for treating neurological (e.g. Alzheimer's) and cardiovascular disorders (e.g. ischaemia).

CC

XX Sequence 628 AA;

SO

QY Query Match 1.5%; Score 8; DB 4; Length 628;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 224 LRVRLKLR 231

3 LRVRLKLR 10
|||||

RESULT 49

ABU21326
ID ABU21326 standard; protein; 789 AA.

XX

AC ABU21326;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #6853.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Burkholderia fungorum.

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

XX

PR 06-SEP-2001; 2001US-00948993.

XX

PR 25-OCT-2001; 2001US-0342923P.

XX

PR 08-FEB-2002; 2002US-00072851.

XX

PR 06-MAR-2002; 2002US-0362699P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003-029926/02.

XX

DR N-PSDB; ACA25196.

XX

PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 49250; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of the 623 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for CC proliferation; (7) identifying a compound that influences the activity of CC the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) CC identifying a gene required for cellular proliferation or the biological CC pathway in which a proliferation-required gene or its gene product lies CC or a gene on which the test compound that inhibits proliferation of an CC organism acts; (9) manufacturing an antibiotic; (10) profiling a CC compound's activity; (11) a culture comprising strains in which the gene CC product is overexpressed or underexpressed; (12) determining the extent CC to which each of the strains is present in a culture or collection of CC strains; or (13) identifying the target of a compound that inhibits the CC proliferation of an organism. The antisense nucleic acids are useful for CC identifying proteins or screening for homologous nucleic acids required CC for cellular proliferation to isolate candidate molecules for rational CC drug discovery programs, or for screening homologous nucleic acids CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*, CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of CC the target prokaryotic essential genes. Note: The sequence data for this CC patent did not form part of the printed specification, but was obtained CC in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

CC

SO Sequence 789 AA;

QY Query Match 1.5%; Score 8; DB 6; Length 789;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 727 LNPDPVFG 734

324 LNPDPVFG 331
|||||

RESULT 50

ADC54146
ID ADC54146 standard; peptide; 13 AA.

XX

AC ADC54146;

XX

DT 18-DEC-2003 (first entry)

XX

DE Peptide linker #1.

XX

KW Peptide linker.

XX

OS Unidentified.

XX

PN JP2003159069-A.

XX

PD 03-JUN-2003.

XX

PF 21-NOV-2001; 2001JP-00356652.

XX

PR 21-NOV-2001; 2001JP-00356652.

XX

PA (KAGA-) KAGAKU GITUTSU SHINKO JIGYODAN.
PA (KOKU-) KOKURITSU YOB0 EISEI KENKYUSHO.

XX

DR WPI; 2003-818676/77.

XX

PT Novel fusion selective marker gene comprising drug-resistance gene CC coupled to reporter gene, useful for manufacturing recombinant proteins.

XX

PS Example 1; Fig 1; 11pp; Japanese.

XX

CC The present invention relates to a fusion selective marker gene (I) CC comprising a drug-resistance gene (II) coupled to a reporter gene (III) CC by a base sequence encoding stuffer amino acid sequence. (II) is a CC puromycin N-acetyl transferase gene (pac) and (III) is an enhanced green CC fluorescent protein (EGFP). (I) is useful for manufacturing recombinant CC protein. (I) is also useful for identifying a desired protein. (II)

CC enables manufacture of recombinant protein, and improved identification
 CC of expression of desired gene. The present sequence is a peptide linker
 CC which was used to illustrate the invention.

XX
 SQ Sequence 13 AA;

Query Match 1.3%; Score 7; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 LEIKLRI 343
 DB 4 LEIKLRI 10

RESULT 51
 AAR72285
 ID AAR72285 standard; peptide; 20 AA.

XX AAR72285;
 AC AAR72285;
 XX 25-MAR-2003 (revised)
 DT 13-NOV-1995 (first entry)
 XX
 DE Glutamic acid decarboxylase (GAD65) fragment.

XX Glutamic acid decarboxylase; GAD65; autoimmune disorders;
 KW insulin-dependant diabetes mellitus; stiff man disease.

XX Homo sapiens.

XX WO9507992-A2.

XX 23-MAR-1995.

XX 24-AUG-1994; 94WO-US009478.

XX 17-SEP-1993; 93US-00123859.

XX (REGC) UNIV CALIFORNIA.

XX Tobin AJ, Erlander MG, Kaufman DL, Claessalzler MJ;

XX WPI; 1995-131360/17.

XX New polypeptide fragments of glutamic acid decarboxylase - for diagnosis
 PT and treatment of auto-immune disease, esp. insulin dependant diabetes,
 PT also related nucleic acid, vectors, antibodies, hybridoma(s) etc.

XX Claim 1; Page 76; 100p; English.

XX A086481 and A086482 encode AAR71733 and AAR79105, rat and human
 CC glutamic acid decarboxylase (GAD65) respectively, from which the GAD65
 CC fragments described in AAR72285-R72298 were derived. These fragments can
 CC be used to detect autoantibodies against GAD, e.g. to diagnose and treat
 CC GAD-related autoimmune disorders, such as insulin dependant diabetes
 CC mellitus or stiff man disease. (Updated on 25-MAR-2003 to correct PN
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 20 AA;

Query Match 1.3%; Score 7; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWKLSGV 233
 DB 9 KWKLSGV 15

RESULT 52
 AAY59556
 ID AAY59556 standard; peptide; 20 AA.

XX AAY59556;
 AC AAY59556;
 XX 03-APR-2000 (first entry)
 DT
 XX
 DE GAD65 fragment, peptide #25.

XX GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KW insulin dependant diabetes mellitus; Stiff man disease; diagnosis;
 KW therapy.

XX Homo sapiens.

XX US598366-A.

XX 07-DEC-1999.

XX 09-APR-1997; 97US-00827618.

XX 21-SEP-1990; 90US-00586536.

XX 18-JUN-1991; 91US-00716909.

XX 07-JUN-1995; 95US-00485725.

XX (REGC) UNIV CALIFORNIA.

XX Tobin AJ, Kaufman DL, Erlander MG;

XX WPI; 2000-095930/08.

XX Ameliorating glutamic acid decarboxylase associated autoimmune disorders
 PT such as insulin dependant diabetes mellitus and Stiffman's disease.

XX Claim 1; Col 42; 61p; English.

XX This sequence represents a fragment of the glutamic acid decarboxylase 65
 CC (GAD65) protein. The invention relates to a method of ameliorating GAD
 CC associated autoimmune disorder by administering a GAD65 peptide to the
 CC patient. The method can be used for ameliorating GAD associated
 CC autoimmune disorders such as IDDM (insulin dependant diabetes mellitus)
 CC and Stiff man disease. GAD65 can also be useful for screening drugs that
 CC alter GAD function, for generating monoclonal antibodies and in
 CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
 CC and the diagnosis is quite easy. It is also possible to obtain much
 CC larger quantities of polypeptide via recombinant techniques than are
 CC available from natural sources

XX Sequence 20 AA;

Query Match 1.3%; Score 7; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWKLSGV 233
 DB 9 KWKLSGV 15

RESULT 53
 ADC54148
 ID ADC54148 standard; peptide; 26 AA.

XX ADC54148;

XX 18-DEC-2003 (first entry)

XX Peptide linker #3.

XX Peptide linker.

XX Unidentified.

XX JP2003159069-A.

PD 03-JUN-2003.
XX
XX 21-NOV-2001; 2001JP-00356652.
XX
XX 21-NOV-2001; 2001JP-00356652.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX (KOKU-) KOKURITSU YOSO EISEI KENKYUSHO.
XX
XX WPI; 2003-818676/77.
XX
XX Novel fusion selective marker gene comprising drug-resistance gene
PT coupled to reporter gene, useful for manufacturing recombinant proteins.
XX
XX Example 1; Fig 1; 11pp; Japanese.
XX
XX The present invention relates to a fusion selective marker gene (I)
CC comprising a drug-resistance gene (II) coupled to a reporter gene (III)
CC by a base sequence encoding stuffer amino acid sequence. (II) is a
CC puromycin N-acetyl transferase gene (pac) and (III) is an enhanced green
CC fluorescent protein (EGFP). (I) is useful for manufacturing recombinant
CC protein. (I) is also useful for identifying a desired protein. (I)
CC enables manufacture of recombinant protein, and improved identification
CC of expression of desired gene. The present sequence is a peptide linker
CC which was used to illustrate the invention.
XX
XX Sequence 26 AA;
SQ
Query Match 1.3%; Score 7; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 337 LEIKRI 343
DB 4 LEIKRI 10
RESULT 54
ADM08067
ID ADM08067 standard; peptide; 32 AA.
XX
XX ADM08067;
AC
XX 20-MAY-2004 (first entry)
DT
XX
XX Canine immunoglobulin group 2 lambda VL species framework 3 peptide 33.
DE
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW antiallergic; allergy; IGE; gene therapy; group 2 lambda species;
KW VL framework; FR3.
XX
XX Canis familiaris.
OS
XX WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
XX Claim 34; Page 102; 130pp; English.
XX
XX The invention relates to a novel canine heavy or light chain variable

CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
XX Sequence 32 AA;
SQ
Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GSSATLT 251
DB 12 GSSATLT 18
RESULT 55
ADM08060
ID ADM08060 standard; peptide; 32 AA.
XX
XX ADM08060;
AC
XX 20-MAY-2004 (first entry)
DT
XX
XX Canine immunoglobulin group 2 lambda VL species framework 3 peptide 26.
DE
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW antiallergic; allergy; IGE; gene therapy; group 2 lambda species;
KW VL framework; FR3.
XX
XX Canis familiaris.
OS
XX WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
XX Claim 34; Page 102; 130pp; English.
XX
XX The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
XX Sequence 32 AA;
SQ
Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GSSATLT 251
DB 12 GSSATLT 18
RESULT 56
ADM07905
ID ADM07905 standard; peptide; 32 AA.

```

XX ADM07905;
AC (IDEX-) IDEXX LAB INC.
XX
XX 20-MAY-2004 (first entry)
DT
DE Canine immunoglobulin group 2 lambda VL genus framework 3 peptide 13.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KM antiallergic; allergy; IGE; gene therapy; group 2 lambda genus;
XX VL framework; FR3.
OS
XX Canis familiaris.
XX
XX WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
XX Claim 33; Page 101; 130pp; English.
XX
XX The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
XX Sequence 32 AA;
SQ
XX
XX Query Match 1.3%; Score 7; DB 7; Length 32;
XX Best Local Similarity 100.0%; Pred. No. 99;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GSSATLT 251
XX |||||
Db 12 GSSATLT 18
XX

RESULT 57
ADM08430
ID ADM08430 standard; peptide; 32 AA.
XX
XX ADM08430;
XX
XX 20-MAY-2004 (first entry)
DT
DE Canine immunoglobulin group 3 VL species framework 3 peptide 15.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KM antiallergic; allergy; IGE; gene therapy; group 3 species; VL framework;
XX FR3.
XX
XX Canis familiaris.
XX
XX WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX

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XX (IDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
XX Claim 40; Page 107; 130pp; English.
XX
XX The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
XX Sequence 32 AA;
SQ
XX
XX Query Match 1.3%; Score 7; DB 7; Length 32;
XX Best Local Similarity 100.0%; Pred. No. 99;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GSSATLT 251
XX |||||
Db 12 GSSATLT 18
XX

RESULT 58
ADM08148
ID ADM08148 standard; peptide; 32 AA.
XX
XX ADM08148;
XX
XX 20-MAY-2004 (first entry)
DT
DE Canine immunoglobulin group 2 lambda VL species framework 3 peptide 43.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KM antiallergic; allergy; IGE; gene therapy; group 2 lambda species;
XX VL framework; FR3.
XX
XX Canis familiaris.
XX
XX WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
XX Claim 34; Page 103; 130pp; English.
XX
XX The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
XX Sequence 32 AA;
SQ

```

Query Match 1.3%; Score 7; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 GSSATLT 251
 |||||
 DB 12 GSSATLT 18

RESULT 59

ADM07907
 ID ADM07907 standard; peptide; 32 AA.

AC ADM07907;

DT 20-MAY-2004 (first entry)

DE Canine immunoglobulin group 2 lambda VL genus framework 3 peptide 15.

KM canine; dog; heavy; immunoglobulin; antibody light chain variable domain;

KM antiallergic; allergy; IGE; gene therapy; group 2 lambda genus;

KM VL framework; FR3.

OS Canis familiaris.

PN WO2003060080-A2.

PD 24-JUL-2003.

PF 20-DEC-2002; 2002WO-US041362.

PR 21-DEC-2001; 2001US-0344874P.

PI (IDEX-) IDEXX LAB INC.

PI Krah ER, Guo H, Aiyappa A, Lawton R;

DR WPI; 2003-598521/56.

PT New canine heavy and light chain variable domain polypeptides, useful for

PT treating canine allergy.

PS Claim 33; Page 101; 130pp; English.

CC The invention relates to a novel canine heavy or light chain variable

CC domain polypeptide. The protein of the invention demonstrates

CC antiallergic activity and may be useful for treating canine allergy,

CC possibly via gene therapy. The current sequence is that of a canine

CC immunoglobulin light chain variable domain framework (FR) peptide of the

SQ Sequence 32 AA;

OY 245 GSSATLT 251
 |||||
 DB 12 GSSATLT 18

RESULT 60

ADM07904
 ID ADM07904 standard; peptide; 32 AA.

AC ADM07904;

DT 20-MAY-2004 (first entry)

DE Canine immunoglobulin group 2 lambda VL genus framework 3 peptide 12.

KM canine; dog; heavy; immunoglobulin; antibody light chain variable domain;

KM antiallergic; allergy; IGE; gene therapy; group 2 lambda genus;

KM VL framework; FR3.

OS Canis familiaris.

PN WO2003060080-A2.

PD 24-JUL-2003.

PF 20-DEC-2002; 2002WO-US041362.

PR 21-DEC-2001; 2001US-0344874P.

PI (IDEX-) IDEXX LAB INC.

PI Krah ER, Guo H, Aiyappa A, Lawton R;

DR WPI; 2003-598521/56.

PT New canine heavy and light chain variable domain polypeptides, useful for

PT treating canine allergy.

PS Claim 33; Page 101; 130pp; English.

CC The invention relates to a novel canine heavy or light chain variable

CC domain polypeptide. The protein of the invention demonstrates

CC antiallergic activity and may be useful for treating canine allergy,

CC possibly via gene therapy. The current sequence is that of a canine

CC immunoglobulin light chain variable domain framework (FR) peptide of the

SQ Sequence 32 AA;

RESULT 61

ADM08347
 ID ADM08347 standard; peptide; 32 AA.

AC ADM08347;

DT 20-MAY-2004 (first entry)

DE Canine immunoglobulin group 3 VL subgenus framework 3 peptide 17.

KM canine; dog; heavy; immunoglobulin; antibody light chain variable domain;

KM antiallergic; allergy; IGE; gene therapy; group 3 subgenus; VL framework;

KM FR3.

OS Canis familiaris.

PN WO2003060080-A2.

PD 24-JUL-2003.

PF 20-DEC-2002; 2002WO-US041362.

PR 21-DEC-2001; 2001US-0344874P.

PI (IDEX-) IDEXX LAB INC.

PI Krah ER, Guo H, Aiyappa A, Lawton R;

DR WPI; 2003-598521/56.

```
PT New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
XX
XX Claim 39; Page 106; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;

Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 62
ADM08348
ID ADM08348 standard; peptide; 32 AA.
XX
XX ADM08348;
XX
XX 20-MAY-2004 (first entry)
XX
DE Canine immunoglobulin group 3 VL subgenus framework 3 peptide 18.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IGE; gene therapy; group 3 subgenus; VL framework;
XX FR3.
XX
XX Canis familiaris.
XX
XX FN WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
XX
XX Claim 39; Page 106; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;

Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 63
ADM08442
ID ADM08442 standard; peptide; 32 AA.
XX
XX ADM08442;
XX
XX 20-MAY-2004 (first entry)
XX
XX Canine immunoglobulin group 3 VL species framework 3 peptide 27.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IGE; gene therapy; group 3 species; VL framework;
XX FR3.
XX
XX Canis familiaris.
XX
XX PN WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
XX
XX Claim 40; Page 107; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;

Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 64
ADM07910
ID ADM07910 standard; peptide; 32 AA.
XX
XX ADM07910;
XX
XX 20-MAY-2004 (first entry)
XX
XX Canine immunoglobulin group 2 lambda VL genus framework 3 peptide 18.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IGE; gene therapy; group 2 lambda genus;
XX VL framework; FR3.
XX
XX Canis familiaris.
XX
XX PN WO2003060080-A2.
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XX 24-JUL-2003.
PD 20-DEC-2002; 2002MO-US041362.
XX 21-DEC-2001; 2001US-0344874P.
XX (IDEX-) IDEXX LAB INC.
PA Krah ER, Guo H, Aiyappa A, Lawton R;
XX WPI; 2003-598521/56.
DR New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
PT Claim 33; Page 101; 130pp; English.
XX The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;
Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GSSATLT 251
DB 12 GSSATLT 18
RESULT 65
ADM08438
ID ADM08438 standard; peptide; 32 AA.
XX ADM08438;
AC 20-MAY-2004 (first entry)
XX DT 20-MAY-2004 (first entry)
XX DE Canine immunoglobulin group 3 VL species framework 3 peptide 23.
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KM antiallergic; allergy; IGE; gene therapy; group 3 species; VL framework;
XX FR3.
XX OS Canis familiaris.
XX PN WO2003060080-A2.
XX PD 24-JUL-2003.
XX PF 20-DEC-2002; 2002MO-US041362.
XX PR 21-DEC-2001; 2001US-0344874P.
XX PA (IDEX-) IDEXX LAB INC.
XX PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX WPI; 2003-598521/56.
DR New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
PT Claim 40; Page 107; 130pp; English.
XX The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates

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```

CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;
Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GSSATLT 251
DB 12 GSSATLT 18
RESULT 66
ADM08062
ID ADM08062 standard; peptide; 32 AA.
XX ADM08062;
AC 20-MAY-2004 (first entry)
XX DT 20-MAY-2004 (first entry)
XX DE Canine immunoglobulin group 2 lambda VL species framework 3 peptide 28.
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KM antiallergic; allergy; IGE; gene therapy; group 2 lambda species;
XX VL framework; FR3.
XX OS Canis familiaris.
XX PN WO2003060080-A2.
XX PD 24-JUL-2003.
XX PF 20-DEC-2002; 2002MO-US041362.
XX PR 21-DEC-2001; 2001US-0344874P.
XX PA (IDEX-) IDEXX LAB INC.
XX PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX WPI; 2003-598521/56.
DR New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
XX PT Claim 34; Page 102; 130pp; English.
XX The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;
Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GSSATLT 251
DB 12 GSSATLT 18
RESULT 67
ADM08336
ID ADM08336 standard; peptide; 32 AA.
XX

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AC ADM08336;
XX
XX 20-MAY-2004 (first entry)
DE Canine immunoglobulin group 3 VL subgenus framework 3 peptide 6.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IgE; gene therapy; group 3 subgenus; VL framework;
XX FR3.
XX
XX Canis familiaris.
XX
XX WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002MO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX PT New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
XX
XX PS Claim 39; Page 106; 130pp; English.
XX
XX The invention relates to a novel canine heavy or light chain variable
XX domain polypeptide. The protein of the invention demonstrates
XX antiallergic activity and may be useful for treating canine allergy,
XX possibly via gene therapy. The current sequence is that of a canine
XX immunoglobulin light chain variable domain framework (FR) peptide of the
XX invention.
XX
XX Sequence 32 AA;
SQ
Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GSSATLT 251
Db |||||
12 GSSATLT 18
RESULT 68
ADA57203
ID ADA57203 standard; protein; 58 AA.
XX
XX ADA57203;
AC
XX 20-NOV-2003 (first entry)
DT
XX Human secreted protein #486.
DE
XX
XX immunosuppressive; antiinflammatory; antiaesthetic; antiallergic;
XX cytoskeletal; cerebroprotective; neuroprotective; nootropic;
XX cardiovascular; antiarteriosclerotic; gene therapy;
XX human secreted protein; immune disorder; inflammation;
XX respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
XX inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
XX multiple sclerosis; ischemic brain injury; Parkinson's disease;
XX Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
XX triple helix formation; antisense gene therapy; forensic biology.
XX
XX Homo sapiens.
XX
XX WO2002102994-A2.
XX

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PD 27-DEC-2002.
XX
XX 19-MAR-2002; 2002MO-US008278.
XX
XX 21-MAR-2001; 2001US-0277340P.
XX
XX 19-JUL-2001; 2001US-0306171P.
XX
XX 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2003-167512/16.
XX
XX N-PSDB; ADA56307.
XX
XX PT New human secreted polypeptides and polynucleotides, useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX conditions, respiratory disorders, cancers, CNS disorders, or
XX neurodegenerative disorders.
XX
XX PS Claim 13; SEQ ID NO 1393; 1754pp; English.
XX
XX The invention relates to 592 new human secreted polypeptides useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX conditions, respiratory disorders, cancers, CNS disorders, or
XX neurodegenerative disorders, or polypeptides comprising an amino acid
XX sequence at least 95% identical to the new sequences. The polypeptides,
XX antibodies or antibody fragments that bind to the polypeptides, nucleic
XX acids encoding the polypeptides, agonists or antagonists that binds to
XX the polypeptide, are useful in preparing diagnostic or pharmaceutical
XX compositions for diagnosing, treating or preventing an e.g. immune
XX disorders, inflammatory conditions (e.g. inflammatory bowel disease,
XX nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
XX allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
XX (e.g. multiple sclerosis or ischemic brain injury), neurodegenerative
XX disorders (e.g. Parkinson's disease or Alzheimer's disease), and
XX cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
XX polynucleotides are useful for chromosome identification, chromosome
XX mapping, for controlling gene expression through triple helix formation
XX or antisense DNA or RNA, in gene therapy, for identifying individuals
XX from minute biological samples, in forensic biology, and as hybridization
XX probes. The polypeptides are useful for as molecular weight markers on
XX sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
XX gels, to raise antibodies, for testing biological activities, and for
XX treating or preventing neural disorders, immune system disorders,
XX muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
XX renal, proliferative and/or cancerous diseases. This sequence corresponds
XX to one of the polypeptide of the invention. Note: The sequence data for
XX this patent did form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 58 AA;
SQ
Query Match 1.3%; Score 7; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 323 AATLDPV 329
Db |||||
43 AATLDPV 49
RESULT 69
ADA41080
ID ADA41080 standard; protein; 58 AA.
XX
XX ADA41080;
AC
XX 20-NOV-2003 (first entry)
DT
XX Human secreted protein.
XX

```

Human; secreted protein; cancer; hyperproliferative disorder;
rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
anaemia; allergic reaction; asthma; cardiovascular disorder;
wound healing; cytostatic; immunosuppressive; neuroprotective;
antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
vulnerary; cardiant; gene therapy.
Homo sapiens.
WO2002102993-A2.
27-DEC-2002.
19-MAR-2002; 2002MO-US008123.
21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Ruben SM;
WPI; 2003-175238/17.
New human secreted proteins and nucleic acid molecules, useful for
preparing a diagnostic or pharmaceutical composition for diagnosing,
preventing or treating cancer or other hyperproliferative disorder,
asthma, allergies or AIDS.
Claim 1; SEQ ID NO 1462; 3205pp; English.
The invention relates to novel genes ADA39629-ADA4055 and proteins
ADA40556-ADA41501 for human secreted proteins, useful for preventing,
treating or ameliorating medical conditions e.g. by protein or gene
therapy. The polypeptides, nucleic acid molecules, antibodies or their
fragments, and agonists or antagonists that bind to the polypeptide are
useful for preparing a diagnostic or pharmaceutical composition for
diagnosing or treating cancer or other hyperproliferative disorder. The
polypeptides and nucleic acid molecules are also useful for detecting,
preventing, diagnosing, prognosticating, treating or ameliorating cancer
or other hyperproliferative disorders including neoplasms, autoimmune
disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
erythematosus, multiple sclerosis, autoimmune thyroiditis or hemolytic
anaemia), haematopoietic or haematological disorders (e.g. anaemia,
thrombocytopenia), allergic reactions including asthma or eczema,
inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
Alzheimer's disease or Parkinson's disease), cardiovascular disorders
(e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
fungal or viral infections including HIV/AIDS), or wound healing and
disorders of epithelial cell proliferation. The nucleic acids are also
useful for chromosome identification, radiation hybrid mapping or long-
range restriction mapping, as molecular weight markers, or as
hybridization or diagnostic probes. The polypeptides and antibodies are
useful for providing immunological probes for differential identification
of the tissues immunohistochemistry assays. Note: The sequence data for
this patent did not form part of the printed specification, but was
obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pcc_sequences.

Query Match 1.3%; Score 7; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 323 ALNLPDV 329
Db 43 ALNLPDV 49

RESULT 70

ABR47918
ID ABR47918 standard; protein; 58 AA.
XX ABR47918;
AC ABR47918;
DT 12-JUN-2003 (first entry)
DE Human secreted protein, SEQ ID 809.
KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
vulnerary; antiinflammatory; neurotropic; neuroprotective;
antiparkinsonian; gene therapy; human; cardiovascular disorder.
Homo sapiens.
WO200295010-A2.
28-NOV-2002.
19-MAR-2002; 2002MO-US009785.
21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Ruben SM;
WPI; 2003-129429/12.
Novel human secreted proteins, useful for detecting, preventing,
diagnosing, prognosticating, treating and/or ameliorating cardiovascular
disorders such as arrhythmia.
Claim 13; SEQ ID NO 809; 1881pp; English.
The present invention relates to novel human secreted proteins (ABR47633-
ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
or their coding sequences are useful for the preparation of a diagnostic
or pharmaceutical composition for diagnosing or treating a cardiovascular
disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
arteriosclerosis and myocardial ischaemia), neural disorders, immune
system disorders, muscular disorders, reproductive disorders,
gastrointestinal disorders, pulmonary disorders, renal disorders,
proliferative disorders and/or cancerous diseases and conditions, for
wound healing and epithelial cell proliferation, to treat inflammation or
infection, for treating thrombosis and arteriosclerosis, for treating or
preventing neural damage which occurs in neuronal disorders or
neurodegenerative conditions such as Alzheimer's disease and Parkinson's
disease, to enhance bone and periodontal regeneration and aid in tissue
transplants or bone grafts, to prevent skin aging or hair loss, to
stimulate growth and differentiation of haematopoietic cells and bone
marrow cells when used in combination with other cytokines, to maintain
organs before transplantation or for supporting cell culture of primary
tissues, to increase or decrease differentiation or proliferation of
embryonic stem cells, or to modulate mammalian characteristics or
metabolism. Note: The sequence data for this patent was published in
electronic format and is available from WIPO at
ftp.wipo.int/pub/published_pcc_sequences

Query Match 1.3%; Score 7; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 323 ALNLPDV 329
Db 43 ALNLPDV 49

RESULT 71

ID	AA	AA36325	standard; protein; 59 AA.
XX	AA	AA36325;	
XX	DT	17-SEP-1999	(first entry)
XX	DE	Human secreted protein encoded by gene 102.	
XX	XX	Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS.	
OS	XX	Homo sapiens.	
XX	PN	MO9931117-A1.	
XX	PD	24-JUN-1999.	
XX	PF	17-DEC-1998; 98MO-US027059.	
XX	PR	18-DEC-1997; 97US-0068006P.	
XX	PR	18-DEC-1997; 97US-0068007P.	
XX	PR	18-DEC-1997; 97US-0068008P.	
XX	PR	18-DEC-1997; 97US-0068009P.	
XX	PR	18-DEC-1997; 97US-0068010P.	
XX	PR	18-DEC-1997; 97US-0068011P.	
XX	PR	18-DEC-1997; 97US-0068012P.	
XX	PR	18-DEC-1997; 97US-0068013P.	
XX	PR	18-DEC-1997; 97US-0068014P.	
XX	PR	18-DEC-1997; 97US-0068015P.	
XX	PR	18-DEC-1997; 97US-0068016P.	
XX	PR	18-DEC-1997; 97US-0068017P.	
XX	PR	18-DEC-1997; 97US-0068018P.	
XX	PR	18-DEC-1997; 97US-0068019P.	
XX	PR	18-DEC-1997; 97US-0068020P.	
XX	PR	18-DEC-1997; 97US-0068021P.	
XX	PR	18-DEC-1997; 97US-0068022P.	
XX	PR	18-DEC-1997; 97US-0068023P.	
XX	PR	18-DEC-1997; 97US-0068024P.	
XX	PR	18-DEC-1997; 97US-0068025P.	
XX	PR	18-DEC-1997; 97US-0068026P.	
XX	PR	18-DEC-1997; 97US-0068027P.	
XX	PR	18-DEC-1997; 97US-0068028P.	
XX	PR	18-DEC-1997; 97US-0068029P.	
XX	PR	18-DEC-1997; 97US-0068030P.	
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XX	PR	18-DEC-1997; 97US-0068033P.	
XX	PR	18-DEC-1997; 97US-0068034P.	
XX	PR	18-DEC-1997; 97US-0068035P.	
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XX	PR	18-DEC-1997; 97US-0068053P.	
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XX	PR	18-DEC-1997; 97US-0068058P.	
XX	PR	18-DEC-1997; 97US-0068059P.	
XX	PR	18-DEC-1997; 97US-0068060P.	
XX	PR	18-DEC-1997; 97US-0068061P.	
XX	PR	18-DEC-1997; 97US-0068062P.	
XX	PR	18-DEC-1997; 97US-0068063P.	
XX	PR	18-DEC-1997; 97US-0068064P.	
XX	PR	18-DEC-1997; 97US-0068065P.	
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XX	PR	18-DEC-1997; 97US-0068067P.	
XX	PR	18-DEC-1997; 97US-0068068P.	
XX	PR	18-DEC-1997; 97US-0068069P.	
XX	PR	18-DEC-1997; 97US-0068070P.	
XX	PR	18-DEC-1997; 97US-0068071P.	
XX	PR	18-DEC-1997; 97US-0068072P.	
XX	PR	18-DEC-1997; 97US-0068073P.	
XX	PR	18-DEC-1997; 97US-0068074P.	
XX	PR	18-DEC-1997; 97US-0068075P.	
XX	PR	18-DEC-1997; 97US-0068076P.	
XX	PR	18-DEC-1997; 97US-0068077P.	
XX	PR	18-DEC-1997; 97US-0068078P.	
XX	PR	18-DEC-1	

[illegible]

CC	represent human secreted proteins, given in the present invention
XX	
SO	Sequence 59 AA;
QY	466 PGFGPTP 472
DB	27 PGFGPTP 33
Query Match	1.3%; Score 7; DB 3; Length 59;
Best Local Similarity	100.0%; Pred.No.1.7e+02;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
RESULT 73	
ADAl1698	
ID	ADAl1698 standard; protein; 59 AA.
AC	
XX	ADAl1698;
XX	
DT	06-NOV-2003 (first entry)
XX	
DE	Human novel secreted protein, SEQ ID NO 226.
XX	
KM	cancer; inflammation; immune disorder; neurological disorder;
KW	blood clotting disorder; food additive; food preservative;
KW	storage capability; fat content; nutritional component; human;
KW	secreted protein.
XX	
OS	Homo sapiens.
XX	
FN	US2003055236-A1.
PD	
XX	20-MAR-2003.
PF	
XX	14-MAR-2002; 2002US-00097065.
PR	
PR	18-DEC-1997; 97US-0068006P.
PR	18-DEC-1997; 97US-0068007P.
PR	18-DEC-1997; 97US-0068008P.
PR	18-DEC-1997; 97US-0068053P.
PR	18-DEC-1997; 97US-0068054P.
PR	18-DEC-1997; 97US-0068064P.
PR	18-DEC-1997; 97US-0070923P.
PR	18-DEC-1997; 97US-0068169P.
PR	19-DEC-1997; 97US-0068365P.
PR	19-DEC-1997; 97US-0068367P.
PR	19-DEC-1997; 97US-0068368P.
PR	19-DEC-1997; 97US-0068369P.
PR	17-DEC-1998; 98MO-US027059.
PR	17-JUN-1999; 99US-00334595.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR;
PI	Kywe H, Wei Y, Florence KA, Duan DR, Florence C, Greene JM, Feng P,
PI	Ferrrie AM, Yu G, Janat F, Ni J;
DR	WI; 2003-567105/53.
DR	N-PSDB; ADAl1574.
XX	
PT	New secreted HKABR24 nucleic acid molecules and polypeptides, useful for
PT	preventing, treating, or ameliorating a medical condition, such as
PT	cancer, inflammation, immune disorders, neurological and blood clotting
PT	disorders.
XX	
PS	Claim 11; SEQ ID NO 226; 11bp; English.
XX	
CC	The invention relates to an isolated HKABR24 nucleic acid molecule. The
CC	polypeptides, nucleic acids and antibodies are useful for diagnosing a
CC	pathological condition or a susceptibility to a pathological condition,
CC	for preventing, treating, or ameliorating a medical condition, such as
CC	cancer, inflammation and other immune disorders, neurological and blood

	CC	cloning disorders. The nucleic acids are also useful for chromosome
	CC	identification, radiation hybrid mapping or long-range restriction
	CC	mapping. The polypeptides and antibodies are useful for providing
	CC	immunological probes for differential identification of the tissues
	CC	immunohistochemistry assays. The polypeptide, polynucleotide, agonist or
	CC	antagonist may also be used as a food additive or preservative to
	CC	increase or decrease storage capabilities, fat content or other
	CC	nutritional components. The present sequence represents the amino acid
	CC	sequence of a novel human secreted protein. Note: The sequence data for
	CC	this patent did not form part of the printed specification but was
	CC	obtained in electronic format directly from USPTO at
	CC	seqdata.uspto.gov.uk/sequence.html?docid=20030055236.
SQ		Sequence 59 AA:
Query Match	1.3%;	Score 7; DB 6; Length 59;
Best Local Similarity	100.0%;	Pred. No. 1.7e+02;
Matches 7; Conservative	0;	Mismatches 0; Indels 0; Gaps 0
QY	323 ALNLPDV 329	
Db	43 ALNLPDV 49	
RESULT 74		
ABP55962		
ID	ABP55962 standard; protein; 63 AA.	
XX		
AC	ABP55962;	
XX		
DT	25-FEB-2003 (first entry)	
XX		
DE	Manduca sexta Fus4 homologue protein SEQ ID NO:77.	
XX		
KM	Antigenic protein; antifungal; haemolymph; fat body; insect larvae;	
XX	plant pathogenic fungi; fungicide; gene therapy; fungal pathogen,	
XX	plant disease resistance; plant fungal disease.	
XX		
XX	Manduca sexta.	
XX		
PN	WO200286072-A2.	
PD		
XX	31-OCT-2002.	
PF	19-APR-2002; 2002MO-US012511.	
XX		
PR	20-APR-2001; 2001US-0285355P.	
XX		
PR	18-APR-2002; 2002US-0012525B.	
XX		
PA	(PION-) PIONEER HI-BRED INT INC.	
XX	(DUPO) DU PONT DE NEMOURS & CO E I.	
PL	Altier DJ, Herrmann R, Lu AJ, McCutchen BF, Presnall JK,	
PI	Weaver JL, Wong JFH,	
XX		
DR	WPI; 2003-075625/O7.	
N-PSDB; ABQ84724.		
FT	New antifungal polypeptides and nucleic acids, useful for enhancing plant	
PT	disease resistance to pathogens, particularly resistance of rice, corn or	
PT	sunflower, to Magnaporthe grisea, Rhizoctonia solani or Fusarium	
PT	verticillioides.	
XX		
PS	Claim 9; Page 122; 142pp; English.	
CC		
CC	The present invention describes antifungal polypeptides (I) isolated from	
CC	the haemolymph and fat bodies of insect larvae induced by injection of	
CC	plant pathogenic fungi. (I) have plant antifungal and fungicide	
CC	activities, and can be used in gene therapy. (I) can be used for	
CC	enhancing plant disease resistance to fungal pathogens, particularly	
CC	resistance of rice, corn, alfalfa, sunflower, Brassica, soybean, cotton,	
CC	safflower, peanut, sorghum, wheat, millet or tobacco to Magnaporthe	
CC	grisea, Rhizoctonia solani or Fusarium verticillioides. This is	

CC particularly useful for controlling plant fungal disease, and lessening
 CC the need for artificial agricultural chemicals to protect field crops and
 CC increase crop yield. (I) may also be used as a pharmaceutical compounds
 CC for treating fungal pathogens in humans and animals. AB084698 to AB084744
 CC and ABP55913 to ABP55992 represent sequence used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 63 AA;

Query March 1.3%; Score 7; DB 6; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 352 VLSTSAV 358
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 Db 14 VLSTSAV 20

RESULT 75

ABP55961
 ID ABP55961 standard; protein; 63 AA.
 XX
 AC ABP55961;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE Manduca sexta Fus4 homologue protein SEQ ID NO:76.
 XX
 KM Antigenic protein; antifungal; haemolymph; fat body; insect larvae;
 KM plant; plant pathogenic fungi; fungicide; gene therapy; fungal pathogen;
 KM plant disease resistance; plant fungal disease.
 OS
 OS Manduca sexta.
 OS
 OS WO200286072-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 19-APR-2002; 2002WO-US012511.
 XX
 PR 20-APR-2001; 2001US-0285355P.
 PR 18-APR-2002; 2002US-00125258.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Altier DJ, Herrmann R, Lu AL, McCutchen BF, Presnail JK;
 PI Weaver DJ, Wong JFH;
 XX
 DR WPI: 2003-075625/07.
 DR N-PSDB; ABQ84724.
 XX
 PT New antifungal polypeptides and nucleic acids, useful for enhancing plant
 PT disease resistance to pathogens, particularly resistance of rice, corn or
 PT sunflower, to Magnaportha grisea, Rhizoctonia solani or Fusarium
 PT verticillioides.
 XX
 PS Claim 9; Page 122; 142pp; English.
 XX
 CC The present invention describes antifungal polypeptides (I) isolated from
 CC the haemolymph and fat bodies of insect larvae induced by injection of
 CC plant pathogenic fungi. (I) have plant antifungal and fungicide
 CC activities, and can be used in gene therapy. (II) can be used for
 CC enhancing plant disease resistance to fungal pathogens, particularly
 CC resistance of rice, corn, alfalfa, sunflower, Brassica, soybean, cotton,
 CC safflower, peanut, sorghum, wheat, millet or tobacco to Magnaportha
 CC grisea, Rhizoctonia solani or Fusarium verticillioides. This is
 CC particularly useful for controlling plant fungal disease, and lessening
 CC the need for artificial agricultural chemicals to protect field crops and
 CC increase crop yield. (I) may also be used as a pharmaceutical compounds
 CC for treating fungal pathogens in humans and animals. AB084698 to AB084744
 CC and ABP55913 to ABP55992 represent sequence used in the exemplification
 CC of the present invention

XX
 SQ Sequence 63 AA;

Query March 1.3%; Score 7; DB 6; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 352 VLSTSAV 358
 |||||
 Db 14 VLSTSAV 20

Search completed: November 16, 2004, 07:27:34
 Job time : 161 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:24:51 ; Search time 142 Seconds

(without alignments)
1300.659 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 522

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Gapop 60.0 , Gapext 60.0

Searched: 1568699 seqs, 353819137 residues

Word size : 0

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5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/PCRUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
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13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	522	100.0	522	14	US-10-245-593-2
3	389	74.5	522	16	US-10-679-246-10
4	330	63.2	522	16	US-10-679-246-8
5	271	51.9	317	15	US-10-264-237-2484
6	231	44.3	231	16	US-10-408-765A-752
7	200	38.3	221	14	US-10-094-749-1723
8	200	38.3	462	10	US-09-397-945-200
9	200	38.3	462	15	US-10-264-237-2485
10	200	38.3	462	15	US-10-653-595-200
11	200	38.3	497	10	US-09-397-945-435
12	200	38.3	497	15	US-10-653-595-435
13	128	24.5	174	10	US-09-397-945-434

14	128	24.5	174	15	US-10-653-595-209	Sequence 209, App
15	128	24.5	174	15	US-10-653-595-434	Sequence 434, App
16	128	24.5	175	10	US-09-397-945-209	Sequence 209, App
17	86	16.5	482	13	US-10-042-417-14	Sequence 14, Appl
18	76	14.6	76	14	US-10-029-386-27908	Sequence 27908, A
19	47	9.0	47	14	US-10-029-386-33496	Sequence 33496, A
20	39	7.5	39	13	US-10-042-417-21	Sequence 21, Appl
21	38	7.3	38	11	US-09-801-348-47	Sequence 47, Appl
22	15	2.9	38	11	US-09-801-348-49	Sequence 49, Appl
23	13	2.5	13	10	US-09-397-945-432	Sequence 432, App
24	13	2.5	13	10	US-09-397-945-433	Sequence 433, App
25	13	2.5	13	15	US-10-653-595-432	Sequence 432, App
26	13	2.5	13	15	US-10-653-595-433	Sequence 433, App
27	8	1.5	57	10	US-09-764-891-2898	Sequence 2898, Ap
28	8	1.5	63	14	US-10-029-386-29488	Sequence 29488, A
29	8	1.5	72	17	US-10-425-115-355684	Sequence 355684,
30	8	1.5	81	15	US-10-424-599-272597	Sequence 272597,
31	8	1.5	89	16	US-10-437-963-142276	Sequence 142276,
32	8	1.5	102	15	US-10-424-599-277325	Sequence 277325,
33	8	1.5	102	17	US-10-425-115-193389	Sequence 193389,
34	8	1.5	117	17	US-10-425-115-122444	Sequence 322444,
35	8	1.5	478	14	US-10-369-483-4506	Sequence 4506, Ap
36	8	1.5	478	14	US-10-369-483-7264	Sequence 7264, Ap
37	8	1.5	628	10	US-09-795-671-5	Sequence 5, Appl1
38	8	1.5	789	15	US-10-282-122A-49250	Sequence 49250, A
39	7	1.3	32	16	US-10-327-598-188	Sequence 188, App
40	7	1.3	32	16	US-10-327-598-190	Sequence 190, App
41	7	1.3	32	16	US-10-327-598-194	Sequence 194, App
42	7	1.3	32	16	US-10-327-598-200	Sequence 200, App
43	7	1.3	32	16	US-10-327-598-201	Sequence 301, App
44	7	1.3	32	16	US-10-327-598-305	Sequence 305, App
45	7	1.3	32	16	US-10-327-598-307	Sequence 307, App
46	7	1.3	36	15	US-10-424-599-184724	Sequence 184724,
47	7	1.3	48	15	US-10-424-599-248433	Sequence 248433,
48	7	1.3	59	14	US-10-097-065-226	Sequence 226, App
49	7	1.3	59	14	US-10-372-876-326	Sequence 876, App
50	7	1.3	60	16	US-10-437-963-115025	Sequence 115025,
51	7	1.3	63	14	US-10-125-288-76	Sequence 76, Appl
52	7	1.3	63	14	US-10-125-288-77	Sequence 77, Appl
53	7	1.3	65	10	US-09-764-891-4887	Sequence 4887, Ap
54	7	1.3	65	15	US-10-424-599-21619	Sequence 21619,
55	7	1.3	65	17	US-10-425-115-280879	Sequence 280879,
56	7	1.3	68	17	US-10-424-599-227458	Sequence 227458,
57	7	1.3	69	17	US-10-425-115-299912	Sequence 299912,
58	7	1.3	72	16	US-10-437-963-138148	Sequence 138148,
59	7	1.3	72	17	US-10-425-115-198211	Sequence 198211,
60	7	1.3	75	16	US-10-767-701-38388	Sequence 38388, A
61	7	1.3	76	15	US-10-424-599-284592	Sequence 284592,
62	7	1.3	78	17	US-10-425-115-192652	Sequence 192652,
63	7	1.3	81	17	US-10-425-115-305666	Sequence 305666,
64	7	1.3	83	15	US-10-424-599-167388	Sequence 167388,
65	7	1.3	83	16	US-10-437-963-200420	Sequence 200420,
66	7	1.3	84	17	US-10-425-115-363121	Sequence 363121,
67	7	1.3	85	16	US-10-437-963-174548	Sequence 174548,
68	7	1.3	86	17	US-10-425-115-313746	Sequence 313746,
69	7	1.3	89	9	US-09-864-761-38560	Sequence 38560, A
70	7	1.3	89	15	US-10-424-599-233924	Sequence 233924,
71	7	1.3	89	16	US-10-437-963-154952	Sequence 154952,
72	7	1.3	90	14	US-10-029-386-34281	Sequence 34281, A
73	7	1.3	92	17	US-10-425-115-306931	Sequence 306931,
74	7	1.3	93	9	US-09-764-860-518	Sequence 518, App
75	7	1.3	93	14	US-10-074-095-518	Sequence 518, App
76	7	1.3	93	14	US-10-219-872-518	Sequence 518, App
77	7	1.3	93	16	US-10-288-122A-71973	Sequence 71973, A
78	7	1.3	93	16	US-10-437-963-162853	Sequence 162853,
79	7	1.3	93	17	US-10-425-115-199612	Sequence 199612,
80	7	1.3	101	10	US-09-764-891-3685	Sequence 3685, Ap
81	7	1.3	101	15	US-10-424-599-254132	Sequence 254132,
82	7	1.3	101	17	US-10-425-115-257044	Sequence 257044,
83	7	1.3	104	17	US-10-425-115-258232	Sequence 258232,
84	7	1.3	107	15	US-10-425-115-255548	Sequence 255548,
85	7	1.3	108	14	US-10-029-386-29734	Sequence 29734, A
86	7	1.3	109	9	US-09-864-761-40024	Sequence 40024, A

87 7 1.3 109 16 US-10-437-963-126759 Sequence 126759,
88 7 1.3 113 16 US-10-767-701-50537 Sequence 50537, A
89 7 1.3 115 15 US-10-434-599-216906 Sequence 216906,
90 7 1.3 116 15 US-10-435-115-359734 Sequence 359734,
91 7 1.3 121 17 US-10-435-115-215265 Sequence 215265,
92 7 1.3 147 15 US-10-437-963-113263 Sequence 113263,
93 7 1.3 147 15 US-10-282-1224-72905 Sequence 72905, A
94 7 1.3 149 17 US-10-435-115-185527 Sequence 185527,
95 7 1.3 149 16 US-10-437-963-198612 Sequence 198612,
96 7 1.3 149 16 US-10-767-701-61039 Sequence 61039, A
97 7 1.3 150 15 US-10-434-599-225222 Sequence 225222,
98 7 1.3 151 16 US-10-437-963-121848 Sequence 121848,
99 7 1.3 151 16 US-10-425-115-278362 Sequence 278362,
100 7 1.3 159 16 US-10-437-963-193530 Sequence 193530,

ALIGNMENTS

RESULT 1
US-09-927-458-2
Sequence 2, Application US/09927458
Patent No. US20020058024A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: KOVALENKO, Andrei
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR F
FILE REFERENCE: WALLACH=22A
CURRENT FILING DATE: 2001-08-13
PCT/IL98/00125
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: IL 120485
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: 09/381,358
PRIOR FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 522
TYPE: PRT
ORGANISM: Homo sapiens
US-09-927-458-2

Query Match 100.0%; Score 522; DB 9; Length 522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLRVLLKRTWPLEVPEPTPTLGHLSRLSLCTWGYSSNTFTITLNYKDPITGDE 60
Db 1 MRLRVLLKRTWPLEVPEPTPTLGHLSRLSLCTWGYSSNTFTITLNYKDPITGDE 60
QY 61 ETLASGYISGDLICILQDDIPAPNIPSTDESHSLQNNQPSLATSSQTSQODEOP 120
Db 61 ETLASGYISGDLICILQDDIPAPNIPSTDESHSLQNNQPSLATSSQTSQODEOP 120
QY 121 SDSFGQAAGSGVWDDMSLGPSONFEASIODNNAHMAEGTGFYSEPMILCSSEVGOVP 180
Db 121 SDSFGQAAGSGVWDDMSLGPSONFEASIODNNAHMAEGTGFYSEPMILCSSEVGOVP 180
QY 181 HSLFTLYGADSDANDALIVLIHILMESGYIPQGTAKALSMPEKMKLSGVYKLYMH 240
Db 181 HSLFTLYGADSDANDALIVLIHILMESGYIPQGTAKALSMPEKMKLSGVYKLYMH 240
QY 241 PLCEGSSATLTCPVLGNLIVNAATLKINNEISVRLQLPPSFICKEKLGENVANITYKD 300
Db 241 PLCEGSSATLTCPVLGNLIVNAATLKINNEISVRLQLPPSFICKEKLGENVANITYKD 300
QY 301 LQKLSRLFKDQIVYPLAFTROALNLPVFGIVLPLELKLRIFRLDVRSVLSAVCR 360
Db 301 LQKLSRLFKDQIVYPLAFTROALNLPVFGIVLPLELKLRIFRLDVRSVLSAVCR 360

QY 361 DLFASNDPLMRFLYLRDPRDNTVRVQDTWKELYRKHIORKESPGRFVMLLPSSSTH 420
Db 361 DLFASNDPLMRFLYLRDPRDNTVRVQDTWKELYRKHIORKESPGRFVMLLPSSSTH 420
QY 421 TTFYVNPMPHPFPFSSRLPFGIGGYDQRTLVYVGPISLLPGCGEETSOFPPLRP 480
Db 421 TTFYVNPMPHPFPFSSRLPFGIGGYDQRTLVYVGPISLLPGCGEETSOFPPLRP 480
QY 481 RDPVGPPLPGPNILPGRGPNDRPFPFSSRGRPTDGRLSFM 522
Db 481 RDPVGPPLPGPNILPGRGPNDRPFPFSSRGRPTDGRLSFM 522

RESULT 2
US-10-245-593-2
Sequence 2, Application US/10245593
Publication No. US20030039646A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: KOVALENKO, Andrei
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR F
FILE REFERENCE: WALLACH=22A
CURRENT FILING DATE: 2002-09-18
PCT/IL98/00125
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: US/09/927,458
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: IL 120485
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: 09/381,358
PRIOR FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 522
TYPE: PRT
ORGANISM: Homo sapiens
US-10-245-593-2

Query Match 100.0%; Score 522; DB 14; Length 522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLRVLLKRTWPLEVPEPTPTLGHLSRLSLCTWGYSSNTFTITLNYKDPITGDE 60
Db 1 MRLRVLLKRTWPLEVPEPTPTLGHLSRLSLCTWGYSSNTFTITLNYKDPITGDE 60
QY 61 ETLASGYISGDLICILQDDIPAPNIPSTDESHSLQNNQPSLATSSQTSQODEOP 120
Db 61 ETLASGYISGDLICILQDDIPAPNIPSTDESHSLQNNQPSLATSSQTSQODEOP 120
QY 121 SDSFGQAAGSGVWDDMSLGPSONFEASIODNNAHMAEGTGFYSEPMILCSSEVGOVP 180
Db 121 SDSFGQAAGSGVWDDMSLGPSONFEASIODNNAHMAEGTGFYSEPMILCSSEVGOVP 180
QY 181 HSLFTLYGADSDANDALIVLIHILMESGYIPQGTAKALSMPEKMKLSGVYKLYMH 240
Db 181 HSLFTLYGADSDANDALIVLIHILMESGYIPQGTAKALSMPEKMKLSGVYKLYMH 240
QY 241 PLCEGSSATLTCPVLGNLIVNAATLKINNEISVRLQLPPSFICKEKLGENVANITYKD 300
Db 241 PLCEGSSATLTCPVLGNLIVNAATLKINNEISVRLQLPPSFICKEKLGENVANITYKD 300
QY 301 LQKLSRLFKDQIVYPLAFTROALNLPVFGIVLPLELKLRIFRLDVRSVLSAVCR 360
Db 301 LQKLSRLFKDQIVYPLAFTROALNLPVFGIVLPLELKLRIFRLDVRSVLSAVCR 360
QY 361 DLFASNDPLMRFLYLRDPRDNTVRVQDTWKELYRKHIORKESPGRFVMLLPSSSTH 420
Db 361 DLFASNDPLMRFLYLRDPRDNTVRVQDTWKELYRKHIORKESPGRFVMLLPSSSTH 420

QY 421 TIFPVNPLHPRPPSRRLPGIIGSYDQPTLPYVGDPISSILPGSGTSPQFPPLRP 480
DB 421 TIFPVNPLHPRPPSRRLPGIIGSYDQPTLPYVGDPISSILPGSGTSPQFPPLRP 480
QY 481 RFDVGVGLPGNPLIPGRGNDPFRPPSRGRPTDRLSFM 522
DB 481 RFDVGVGLPGNPLIPGRGNDPFRPPSRGRPTDRLSFM 522

RESULT 3

US-10-679-246-10
; Sequence 10, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: In Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 10
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-10

Query Match 74.5%; Score 389; DB 16; Length 522;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 489; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33 SLCTWGYSSNTRTITLANKDPLTGDEETLASYGISDILICILDDIPAPNIPESD 92
DB 33 SLCTWGYSSNTRTITLANKDPLTGDEETLASYGISDILICILDDIPAPNIPESD 92
QY 93 SEHSIQLNNEQPSLATSSNOTSMODEQPSDFQQAAGSVWMDSMLGPSQNEFEASI 152
DB 93 SEHSIQLNNEQPSLATSSNOTSMODEQPSDFQQAAGSVWMDSMLGPSQNEFEASI 152
QY 153 DNAMAAGTGFPSEBPMCSSEVGOVPHSLETTYQSADCSANDALIVLHLMESGY 212
DB 153 DNAMAAGTGFPSEBPMCSSEVGOVPHSLETTYQSADCSANDALIVLHLMESGY 212
QY 213 IPOGTEAKALMPKMKLSGYKLYQWMPLECGSSATLTCVPLGNLIVNATLKINNEI 272
DB 213 IPOGTEAKALMPKMKLSGYKLYQWMPLECGSSATLTCVPLGNLIVNATLKINNEI 272
QY 273 SVKSLQLLPESFICKKELGENVANITYKDLQKLSLFDQVLYPLAFTROALNLPVFG 332
DB 273 SVKSLQLLPESFICKKELGENVANITYKDLQKLSLFDQVLYPLAFTROALNLPVFG 332
QY 333 VVLPLELKLRIFRLLDVRSVLSAVGRDLFTASNDPLMRFLLYLRDFTVAVQDTW 392
DB 333 VVLPLELKLRIFRLLDVRSVLSAVGRDLFTASNDPLMRFLLYLRDFTVAVQDTW 392
QY 393 KELYRKRIQRKESPKGRFVWLTPSSTHTIFFYNNPLHPRPPSSRLPGIIGSEYQRP 452
DB 393 KELYRKRIQRKESPKGRFVWLTPSSTHTIFFYNNPLHPRPPSSRLPGIIGSEYQRP 452
QY 453 TLPIVGDPISSILIPGGETPSQFPPLRFPVGPPLRQPNILPGRGNDPFRPPSRG 512
DB 453 TLPIVGDPISSILIPGGETPSQFPPLRFPVGPPLRQPNILPGRGNDPFRPPSRG 512
QY 513 RPTDGRLSFM 522
DB 513 RPTDGRLSFM 522

RESULT 4

US-10-679-246-8
; Sequence 8, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: In Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-8

Query Match 63.2%; Score 330; DB 16; Length 443;
Best Local Similarity 99.8%; Pred. No. 6,4e-298;
Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 92 DEHSIQLNNEQPSLATSSNOTSMODEQPSDFQQAAGSVWMDSMLGPSQNEFEASI 151
DB 13 DEHSIQLNNEQPSLATSSNOTSMODEQPSDFQQAAGSVWMDSMLGPSQNEFEASI 72
QY 152 DNAMAAGTGFPSEBPMCSSEVGOVPHSLETTYQSADCSANDALIVLHLMESGY 211
DB 73 DNAMAAGTGFPSEBPMCSSEVGOVPHSLETTYQSADCSANDALIVLHLMESGY 132
QY 212 YIPOGTEAKALMPKMKLSGYKLYQWMPLECGSSATLTCVPLGNLIVNATLKINNEI 271
DB 133 YIPOGTEAKALMPKMKLSGYKLYQWMPLECGSSATLTCVPLGNLIVNATLKINNEI 192
QY 272 RSVKRLQLLPESFICKKELGENVANITYKDLQKLSLFDQVLYPLAFTROALNLPVFG 331
DB 193 RSVKRLQLLPESFICKKELGENVANITYKDLQKLSLFDQVLYPLAFTROALNLPVFG 252
QY 332 VVLPLELKLRIFRLLDVRSVLSAVGRDLFTASNDPLMRFLLYLRDFTVAVQDTW 391
DB 253 VVLPLELKLRIFRLLDVRSVLSAVGRDLFTASNDPLMRFLLYLRDFTVAVQDTW 312
QY 392 WKELYRKRIQRKESPKGRFVWLTPSSTHTIFFYNNPLHPRPPSSRLPGIIGSEYQRP 451
DB 313 WKELYRKRIQRKESPKGRFVWLTPSSTHTIFFYNNPLHPRPPSSRLPGIIGSEYQRP 372
QY 452 TLPIVGDPISSILIPGGETPSQFPPLRFPVGPPLRQPNILPGRGNDPFRPPSRG 511
DB 373 TLPIVGDPISSILIPGGETPSQFPPLRFPVGPPLRQPNILPGRGNDPFRPPSRG 432
QY 512 GRPTDGRLSFM 522
DB 433 GRPTDGRLSFM 443

RESULT 5

US-10-264-237-2484
; Sequence 2484, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876

SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO: 2484
LENGTH: 317
TYPE: PRF
ORGANISM: Homo sapiens
US-10-264-237-2484

Query Match 51.9%; Score 271; DB 15; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.5e-243;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 LGSQNFPAESIIONAHMAEGTGFPSPMLCSSEBEGOVHSHETTYQASDGDNDAL 199
DB 26 LGSQNFPAESIIONAHMAEGTGFPSPMLCSSEBEGOVHSHETTYQASDGDNDAL 85
QY 200 IYLHLMLESYIPQGTAKALSMPEKMLSGYKQLQYHMLPGSSSATLTCTPLGNLI 259
DB 86 IYLHLMLESYIPQGTAKALSMPEKMLSGYKQLQYHMLPGSSSATLTCTPLGNLI 145
QY 260 VVNATLKINNEIRSVKRIQLPESFICEKLGENVANIKDQLSRLFKDQLYPLIAF 319
DB 146 VVNATLKINNEIRSVKRIQLPESFICEKLGENVANIKDQLSRLFKDQLYPLIAF 205
QY 320 TROALNLPDVGVLVPLLEKLRIFRLLDVAVSLSAVCRDLFTASNDPLMRFYLARD 379
DB 206 TROALNLPDVGVLVPLLEKLRIFRLLDVAVSLSAVCRDLFTASNDPLMRFYLARD 265
QY 380 FRDNTVRVODTDWKLKRYKRRIQRKESPKGR 410
DB 266 FRDNTVRVODTDWKLKRYKRRIQRKESPKGR 296

RESULT 6
US-10-408-765A-752

Sequence 752, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Faby, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 752
LENGTH: 231
TYPE: PRF
ORGANISM: Homo sapiens
US-10-408-765A-752

Query Match 44.3%; Score 231; DB 16; Length 231;
Best Local Similarity 100.0%; Pred. No. 4.2e-206;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 ENVANITYKDLQSLFLFKDQLYPLIATTRQALNLPDVGVLVPLLEKLRIFRLDVS 351
DB 1 ENVANITYKDLQSLFLFKDQLYPLIATTRQALNLPDVGVLVPLLEKLRIFRLDVS 60
QY 352 VLSLAVCRDLFTASNDPLMRFYLARDPFRONTVRVODTDWKLKRYKRRIQRKESPKGRF 411
DB 61 VLSLAVCRDLFTASNDPLMRFYLARDPFRONTVRVODTDWKLKRYKRRIQRKESPKGRF 120
QY 412 VMLPSSHTIIPFYNPLHPRPFPSSRLPGIIGGEYDQRTLPYVGPPISSSLIPGGGT 471
DB 121 VMLPSSHTIIPFYNPLHPRPFPSSRLPGIIGGEYDQRTLPYVGPPISSSLIPGGGT 180

QY 472 PSQFPELRPRDPVGBLPQPNFILPGRGGPNDRPFPRSGRPTDGRISFM 522
DB 181 PSQFPELRPRDPVGBLPQPNFILPGRGGPNDRPFPRSGRPTDGRISFM 231

RESULT 7
US-10-094-749-1723

Sequence 1723, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAYASU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOMYUKI
APPLICANT: NAGAHARA, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1723
LENGTH: 221
TYPE: PRF
ORGANISM: Homo sapiens
US-10-094-749-1723

Query Match 38.3%; Score 200; DB 14; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.8e-177;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 AMLPDPVGLVPLLEKLRIFRLLDVRSVLSAVCRDLFTASNDPLMRLYLARDPD 382
DB 22 AMLPDPVGLVPLLEKLRIFRLLDVRSVLSAVCRDLFTASNDPLMRLYLARDPD 81
QY 383 NTVRVODTDWKLKRYKRRIQRKESPKGRFVMLPSTHTIIPYPNPLHPRPFPSSRLPFG 442
DB 82 NTVRVODTDWKLKRYKRRIQRKESPKGRFVMLPSTHTIIPYPNPLHPRPFPSSRLPFG 141
QY 443 IIGGEYDQRTLPYVGPPISSSLIPGGGTSGFPPLRPDPVGBLPQPNFILPGRGPN 502
DB 142 IIGGEYDQRTLPYVGPPISSSLIPGGGTSGFPPLRPDPVGBLPQPNFILPGRGPN 201
QY 503 DRPFRPSRGRPTDGRISFM 522
DB 202 DRPFRPSRGRPTDGRISFM 221

RESULT 8
US-09-397-945-200

Sequence 200, Application US/09397945
Publication No. US20030065139A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1

```

; CURRENT APPLICATION NUMBER: US/09/397,945
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-397-945-200

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Query Match 38.3%; Score 200; DB 10; Length 462;

Best Local Similarity 100.0%; Pred. No. 5.2e-177; Indels 0; Gaps 0;

Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 323 ALNLPDVGVLVLPLELKRIFRLDVRSVLSAVCRDLFTASNDPLMRFLYLRDPRD 382
DB 263 ALNLPDVGVLVLPLELKRIFRLDVRSVLSAVCRDLFTASNDPLMRFLYLRDPRD 322
QY 383 NTVAVQDTWKELYRKRIQRKESPKGRFVWLLPSSHTTIPFPNPLHPPFPSSRLPPG 442
DB 323 NTVAVQDTWKELYRKRIQRKESPKGRFVWLLPSSHTTIPFPNPLHPPFPSSRLPPG 382
QY 443 IIGGEYDQRPFLPYVGDPISSILPGGETPSQFPPLRPDPVGLPGNPIILPGRGGN 502
DB 383 IIGGEYDQRPFLPYVGDPISSILPGGETPSQFPPLRPDPVGLPGNPIILPGRGGN 442
QY 503 DRPFPRPSRGRPTDGRLSFM 522
DB 443 DRPFPRPSRGRPTDGRLSFM 462

RESULT 9
US-10-264-237-2485
; Sequence 2485, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Bize et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18

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; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2485
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2485

```

Query Match 38.3%; Score 200; DB 15; Length 462;

Best Local Similarity 100.0%; Pred. No. 5.2e-177; Indels 0; Gaps 0;

Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 323 ALNLPDVGVLVLPLELKRIFRLDVRSVLSAVCRDLFTASNDPLMRFLYLRDPRD 382
DB 263 ALNLPDVGVLVLPLELKRIFRLDVRSVLSAVCRDLFTASNDPLMRFLYLRDPRD 322
QY 383 NTVAVQDTWKELYRKRIQRKESPKGRFVWLLPSSHTTIPFPNPLHPPFPSSRLPPG 442
DB 323 NTVAVQDTWKELYRKRIQRKESPKGRFVWLLPSSHTTIPFPNPLHPPFPSSRLPPG 382
QY 443 IIGGEYDQRPFLPYVGDPISSILPGGETPSQFPPLRPDPVGLPGNPIILPGRGGN 502
DB 383 IIGGEYDQRPFLPYVGDPISSILPGGETPSQFPPLRPDPVGLPGNPIILPGRGGN 442
QY 503 DRPFPRPSRGRPTDGRLSFM 522
DB 443 DRPFPRPSRGRPTDGRLSFM 462

```

RESULT 10

US-10-653-595-200

; Sequence 200, Application US/10653595

; Publication No. US20040048304A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et. al.

; TITLE OF INVENTION: 95 Human secreted proteins

; FILE REFERENCE: P2027P1C1

; CURRENT APPLICATION NUMBER: US/10/653,595

; CURRENT FILING DATE: 2003-09-03

; PRIOR APPLICATION NUMBER: US 09/397945

; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: PCT/US99/05804

; PRIOR FILING DATE: 1999-03-18

; PRIOR APPLICATION NUMBER: 60/078,566

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,576

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,573

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,574

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,579

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/080,314

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/080,312

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/078,578

; PRIOR FILING DATE: 1998-03-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 470

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 200

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

NAME/KEY: SITE
LOCATION: (115)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-653-595-200

Query Match 38.3%; Score 200; DB 15; Length 462;
Best Local Similarity 100.0%; Pred. No. 5.2e-177; Indels 0; Gaps 0;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDVGVLVPLELKLRIPLRLDVSYSLSAVCDLFTASNDPLLMRFYLDRDRD 382
DB 263 ALNLPDVGVLVPLELKLRIPLRLDVSYSLSAVCDLFTASNDPLLMRFYLDRDRD 322
QY 323 NTVRVQDIDWKELRKRIQRKESPKGFVWLLPSSHTTIPYPNPLHPPSPSRLLPG 442
DB 323 NTVRVQDIDWKELRKRIQRKESPKGFVWLLPSSHTTIPYPNPLHPPSPSRLLPG 382
QY 443 IIGGEYDQPTLPYVGPDISSLIIPGGETPSQFPPLRFPDVGPLPGPNPLPGRGPN 502
DB 383 IIGGEYDQPTLPYVGPDISSLIIPGGETPSQFPPLRFPDVGPLPGPNPLPGRGPN 442
QY 503 DRFPFRPSRGPRPTDGRLSFM 522
DB 443 DRFPFRPSRGPRPTDGRLSFM 462

RESULT 11

US-09-397-945-435
Sequence 435, Application US/09397945
Publication No. US20030065139A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1
CURRENT FILING DATE: US/09/397,945
PRIOR FILING DATE: 1998-03-17, 945
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,581
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,577
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,563
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,313
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 470
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 435
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1150)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-397-945-435

Query Match 38.3%; Score 200; DB 10; Length 497;
Best Local Similarity 100.0%; Pred. No. 5.6e-177; Indels 0; Gaps 0;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDVGVLVPLELKLRIPLRLDVSYSLSAVCDLFTASNDPLLMRFYLDRDRD 382
DB 298 ALNLPDVGVLVPLELKLRIPLRLDVSYSLSAVCDLFTASNDPLLMRFYLDRDRD 357
QY 383 NTVRVQDIDWKELRKRIQRKESPKGFVWLLPSSHTTIPYPNPLHPPSPSRLLPG 442
DB 358 NTVRVQDIDWKELRKRIQRKESPKGFVWLLPSSHTTIPYPNPLHPPSPSRLLPG 417
QY 443 IIGGEYDQPTLPYVGPDISSLIIPGGETPSQFPPLRFPDVGPLPGPNPLPGRGPN 502
DB 418 IIGGEYDQPTLPYVGPDISSLIIPGGETPSQFPPLRFPDVGPLPGPNPLPGRGPN 477
QY 503 DRFPFRPSRGPRPTDGRLSFM 522
DB 478 DRFPFRPSRGPRPTDGRLSFM 497

RESULT 12

US-10-653-595-435
Sequence 435, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1
CURRENT FILING DATE: US/10/653,595
CURRENT FILING DATE: 2003-09-03
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: US 09/397945
PRIOR FILING DATE: 1998-03-18
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 435
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (150)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-653-595-435

Query Match 38.3%; Score 200; DB 15; Length 497;
Best Local Similarity 100.0%; Pred. No. 5.6e-177; Indels 0; Gaps 0;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDVGVLVPLELKLRIPLRLDVSYSLSAVCDLFTASNDPLLMRFYLDRDRD 382
DB 298 ALNLPDVGVLVPLELKLRIPLRLDVSYSLSAVCDLFTASNDPLLMRFYLDRDRD 357

QY 383 NTWVQDPTWKEIYRKXHIQKESPKGRFVMLPSSSTHTIFPYPNLHPRFPSSRLPG 442
DB 358 NTWVQDPTWKEIYRKXHIQKESPKGRFVMLPSSSTHTIFPYPNLHPRFPSSRLPG 417
QY 443 IIGGEYDQRTPLFYVGPDISLIPGGEPTSPFPPLRPDPVGPLPGPNPILPGRGPN 502
DB 418 IIGGEYDQRTPLFYVGPDISLIPGGEPTSPFPPLRPDPVGPLPGPNPILPGRGPN 477
QY 503 DRFPFRSRGRPTDGRLSFM 522
DB 478 DRFPFRSRGRPTDGRLSFM 497

RESULT 13
US-09-397-945-434
Sequence 434, Application US/09397945
Publication No. US20030065139A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1
CURRENT APPLICATION NUMBER: US/09/397,945
PRIORITY FILING DATE: 1999-09-17
PRIORITY APPLICATION NUMBER: PCT/US99/05804
PRIORITY FILING DATE: 1999-03-18
PRIORITY APPLICATION NUMBER: 60/078,566
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,576
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,573
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,574
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,579
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/080,314
PRIORITY FILING DATE: 1998-04-01
PRIORITY APPLICATION NUMBER: 60/080,312
PRIORITY FILING DATE: 1998-04-01
PRIORITY APPLICATION NUMBER: 60/078,578
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,581
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,577
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,563
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/080,313
PRIORITY FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 434
LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
US-09-397-945-434

Query Match 24.5%; Score 128; DB 10; Length 174;
Best Local Similarity 100.0%; Pred. No. 2e-110;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 395 LYRKXHIQKESPKGRFVMLPSSSTHTIFPYPNLHPRFPSSRLPGIIGGEYDQRTPL 454
DB 47 LYRKXHIQKESPKGRFVMLPSSSTHTIFPYPNLHPRFPSSRLPGIIGGEYDQRTPL 106
QY 455 PYVGPDISLIPGGEPTSPFPPLRPDPVGPLPGPNPILPGRGPNDRFPFRSRGRP 514
DB 107 PYVGPDISLIPGGEPTSPFPPLRPDPVGPLPGPNPILPGRGPNDRFPFRSRGRP 166
QY 515 TDGRLSFM 522
DB 167 TDGRLSFM 174

RESULT 14
US-10-653-595-209
Sequence 209, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1
CURRENT APPLICATION NUMBER: US/10/653,595
PRIORITY FILING DATE: 2003-09-03
PRIORITY APPLICATION NUMBER: US 09/397945
PRIORITY FILING DATE: 1999-09-17
PRIORITY APPLICATION NUMBER: PCT/US99/05804
PRIORITY FILING DATE: 1999-03-18
PRIORITY APPLICATION NUMBER: 60/078,566
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,576
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,573
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,574
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,579
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/080,314
PRIORITY FILING DATE: 1998-04-01
PRIORITY APPLICATION NUMBER: 60/080,312
PRIORITY FILING DATE: 1998-04-01
PRIORITY APPLICATION NUMBER: 60/078,578
PRIORITY FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 209
LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
US-10-653-595-209

Query Match 24.5%; Score 128; DB 15; Length 174;
Best Local Similarity 100.0%; Pred. No. 2e-110;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 LYRKXHIQKESPKGRFVMLPSSSTHTIFPYPNLHPRFPSSRLPGIIGGEYDQRTPL 454
DB 47 LYRKXHIQKESPKGRFVMLPSSSTHTIFPYPNLHPRFPSSRLPGIIGGEYDQRTPL 106
QY 455 PYVGPDISLIPGGEPTSPFPPLRPDPVGPLPGPNPILPGRGPNDRFPFRSRGRP 514
DB 107 PYVGPDISLIPGGEPTSPFPPLRPDPVGPLPGPNPILPGRGPNDRFPFRSRGRP 166
QY 515 TDGRLSFM 522
DB 167 TDGRLSFM 174
RESULT 15
US-10-653-595-434
Sequence 434, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1
CURRENT APPLICATION NUMBER: US/10/653,595
PRIORITY FILING DATE: 2003-09-03
PRIORITY APPLICATION NUMBER: US 09/397945
PRIORITY FILING DATE: 1999-09-17
PRIORITY APPLICATION NUMBER: PCT/US99/05804
PRIORITY FILING DATE: 1998-03-18
PRIORITY APPLICATION NUMBER: 60/078,566
PRIORITY FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 434
LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
US-10-653-595-434

Query Match 24.5% Score 128; DB 15; Length 174;
Best Local Similarity 100.0%; Pred. No. 2e-110;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 LYRKHIQKESPKGRFVWLPSSTHTIPFYPNPLHPPSPSSRLPGIIGEXYDQPTL 454
DB 47 LYRKHIQKESPKGRFVWLPSSTHTIPFYPNPLHPPSPSSRLPGIIGEXYDQPTL 106
QY 455 PYVGPDISLIPGGETTSQFPPLRPDPVGPPLPGGPNDRPFPSPGRP 514
DB 107 PYVGPDISLIPGGETTSQFPPLRPDPVGPPLPGGPNDRPFPSPGRP 166
QY 515 TDGRUSFM 522
DB 167 TDGRUSFM 174

RESULT 16
US-09-397-945-209
Sequence 209, Application US/09397945
Publication No. US20030065139A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: 35 Human secreted proteins
FILE REFERENCE: P2027P1
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,581
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,577
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,563

PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,313
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 209
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (175)
OTHER INFORMATION: Xaa equals stop translation
US-09-397-945-209

Query Match 24.5% Score 128; DB 10; Length 175;
Best Local Similarity 100.0%; Pred. No. 2e-110;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 LYRKHIQKESPKGRFVWLPSSTHTIPFYPNPLHPPSPSSRLPGIIGEXYDQPTL 454
DB 47 LYRKHIQKESPKGRFVWLPSSTHTIPFYPNPLHPPSPSSRLPGIIGEXYDQPTL 106
QY 455 PYVGPDISLIPGGETTSQFPPLRPDPVGPPLPGGPNDRPFPSPGRP 514
DB 107 PYVGPDISLIPGGETTSQFPPLRPDPVGPPLPGGPNDRPFPSPGRP 166
QY 515 TDGRUSFM 522
DB 167 TDGRUSFM 174

RESULT 17
US-10-042-417-14
Sequence 14, Application US/10042417
Publication No. US20020123082A1
GENERAL INFORMATION:
APPLICANT: Pacano, M.
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-5
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 482
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-14

Query Match 16.5% Score 86; DB 13; Length 482;
Best Local Similarity 100.0%; Pred. No. 5.6e-71;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LCEGSSATLTCTVPLGNLIVNATLTKINNEISVYRIQLPSPTCKEKLGENVANIYKDL 301
DB 202 LCEGSSATLTCTVPLGNLIVNATLTKINNEISVYRIQLPSPTCKEKLGENVANIYKDL 261
QY 302 QXLSRLFKDQIVYPLAFTROALNLP 327
DB 262 QXLSRLFKDQIVYPLAFTROALNLP 287

RESULT 18
US-10-029-386-27908
Sequence 27908, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn. Sharron G.
APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 27908
LENGTH: 76
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR22.55.0
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2
OTHER INFORMATION: SWISSPROT HIT: Q9Y311, EVALU 5.00e-39
US-10-029-386-27908

Query Match 14.6%; Score 76; DB 14; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.3e-62;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 LGPSONEFEASIODNMAHEGTGFPSEPMLCSESVGCVPSLETLYOSADCSNDAL 199
Db 1 LGPSONEFEASIODNMAHEGTGFPSEPMLCSESVGCVPSLETLYOSADCSNDAL 60
QY 200 IVLIHLMLESGYIPQ 215
Db 61 IVLIHLMLESGYIPQ 76

RESULT 19
US-10-029-386-33496
Sequence 33496, Application US/100293386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33496
LENGTH: 47
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL035068.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: SWISSPROT HIT: Q9Y311, EVALU 5.00e-22
US-10-029-386-33496

Query Match 9.0%; Score 47; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.4e-35;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 GTEKALSMPEKMLSGVYKQVHNPCESSATLTCTVPLGNLIVN 262
Db 1 GTEKALSMPEKMLSGVYKQVHNPCESSATLTCTVPLGNLIVN 47

RESULT 20
US-10-042-417-21

Sequence 21, Application US/10042417
Publication No. US20020123082A1
GENERAL INFORMATION:
APPLICANT: Pagano, M.
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIORITY FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-21

Query Match 7.5%; Score 39; DB 13; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPELKLRIIFRLIDVRSVLSAVCRDLFTASNDPLMR 373
Db 1 LPELKLRIIFRLIDVRSVLSAVCRDLFTASNDPLMR 39

RESULT 21
US-09-801-348-47
Sequence 47, Application US/09801348
Publication No. US20040166530A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Elledge, Stephen J.
TITLE OF INVENTION: P-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/801,348
CURRENT FILING DATE: 2001-07-31
EARLIER APPLICATION NUMBER: 09/172,841
EARLIER FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 47
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-801-348-47

Query Match 7.3%; Score 38; DB 11; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPELKLRIIFRLIDVRSVLSAVCRDLFTASNDPLMR 372
Db 1 LPELKLRIIFRLIDVRSVLSAVCRDLFTASNDPLMR 38

RESULT 22
US-09-801-348-49
Sequence 49, Application US/09801348
Publication No. US20040166530A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Elledge, Stephen J.
TITLE OF INVENTION: P-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/801,348
CURRENT FILING DATE: 2001-07-31
EARLIER APPLICATION NUMBER: 09/172,841
EARLIER FILING DATE: 1998-10-15

```
;; EARLIER APPLICATION NUMBER: 08/951,621
;; EARLIER FILING DATE: 1997-10-16
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 49
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-801-348-49
```

```
Query Match      2.9%; Score 15; DB 11; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      335 LPLEIKRIFRLDV 349
DB      1 LPLEIKRIFRLDV 15
```

```
RESULT 23
US-09-397-945-432
; Sequence 432, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 432
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-945-432
```

```
Query Match      2.5%; Score 13; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      308 FKQQLVYFLAFT 320
DB      1 FKQQLVYFLAFT 13
```

RESULT 24

```
US-09-397-945-433
; Sequence 433, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 433
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-945-433
```

```
Query Match      2.5%; Score 13; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      321 RQALNLPDYFGLV 333
DB      1 RQALNLPDYFGLV 13
```

```
RESULT 25
US-10-653-595-432
; Sequence 432, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1C1
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US/09/397945
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
```


PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 432
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-653-595-432

Query Match 2.5%; Score 13; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 FKQDLYVPLAFT 320
Db 1 FKQDLYVPLAFT 13

RESULT 26
US-10-653-595-433
Sequence 433, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1C1
CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: US 09/397945
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 433
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-653-595-433

Query Match 2.5%; Score 13; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 ROALNLPDVFGLV 333
Db 1 ROALNLPDVFGLV 13

RESULT 27
US-09-764-891-2898
Sequence 2898, Application US/09764891
Publication No. US2003007808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P2006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2898
LENGTH: 57
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-891-2898

Query Match 1.5%; Score 8; DB 10; Length 57;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 SPKGRFVM 413
Db 1 SPKGRFVM 8

RESULT 28
US-10-029-386-29488
Sequence 29488, Application US/10029386
Publication No. US2003019470A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Penn, Sharon G.
APPLICANT: Hank, David R.
APPLICANT: Hankel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CH
FILE REFERENCE: A60MICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 29488
LENGTH: 63
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHRA.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.45
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.59
OTHER INFORMATION: SWISSPROT HIT: P22599, EVALUATE 1.60e+00
US-10-029-386-29488

Query Match 1.5%; Score 8; DB 14; Length 63;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 RSVLSLSA 357
Db 32 RSVLSLSA 39

RESULT 29
US-10-425-115-355684
Sequence 355684, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.

```

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 355684
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_87549C.1.pep
US-10-425-115-355684

Query Match
Best Local Similarity 1.5%; Score 8; DB 17; Length 72;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 LIVLHLL 206
DB 39 LIVLHLL 46

RESULT 30
US-10-424-599-272597
; Sequence 272597, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 272597
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_88177C.1.pep
US-10-424-599-272597

Query Match
Best Local Similarity 1.5%; Score 8; DB 15; Length 81;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 PETEPTLG 24
DB 58 PETEPTLG 65

RESULT 31
US-10-437-963-142276
; Sequence 142276, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
```

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; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142276
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43298C.1.pep
US-10-437-963-142276

Query Match
Best Local Similarity 1.5%; Score 8; DB 16; Length 89;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 ILPGRGSP 501
DB 55 ILPGRGSP 62

RESULT 32
US-10-424-599-277325
; Sequence 277325, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 277325
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(102)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_92448C.1.pep
US-10-424-599-277325

Query Match
Best Local Similarity 1.5%; Score 8; DB 15; Length 102;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 FRDNTVRV 387
DB 43 FRDNTVRV 50

RESULT 33
US-10-425-115-193389
; Sequence 193389, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 193389
; LENGTH: 102
```

TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MFT4577_107956C.1.pcp
US-10-425-115-193389

Query Match
Best Local Similarity 100.0%; Score 8; DB 17; Length 102;
Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 LRIPLD 348
Db 41 LRIPLD 48

RESULT 34
US-10-425-115-32244
Sequence 32244, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yinhua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 322444
LENGTH: 117
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MFT4577_57133C.1.pcp
US-10-425-115-322444

Query Match
Best Local Similarity 100.0%; Score 8; DB 17; Length 117;
Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 VRSVLS 356
Db 57 VRSVLS 64

RESULT 35
US-10-369-493-4506
Sequence 4506, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4506
LENGTH: 478
TYPE: PRT
ORGANISM: Burkholderia fungorum
US-10-369-493-4506

Query Match
Best Local Similarity 100.0%; Score 8; DB 14; Length 478;
Pred. No. 1.9e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 216 GTEAKLS 223
Db 388 GTEAKLS 395

RESULT 36
US-10-369-493-7264
Sequence 7264, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7264
LENGTH: 478
TYPE: PRT
ORGANISM: Burkholderia cepacia
US-10-369-493-7264

Query Match
Best Local Similarity 100.0%; Score 8; DB 14; Length 478;
Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 GTEAKLS 223
Db 388 GTEAKLS 395

RESULT 37
US-09-795-671-5
Sequence 5, Application US/09795671
Publication No. US20030207347A1
GENERAL INFORMATION:
APPLICANT: Burgeson, Robert
APPLICANT: Brunken, William
APPLICANT: Koch, Manuel
APPLICANT: Hunter, Dale
APPLICANT: Olson, Pamela
TITLE OF INVENTION: BETA NITRIN AND USES THEREOF
FILE REFERENCE: 10287-057001
CURRENT APPLICATION NUMBER: US/09/795,671
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/185,811
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 60/229,893
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 628
TYPE: PRT
ORGANISM: Mus musculus
US-09-795-671-5

Query Match
Best Local Similarity 100.0%; Score 8; DB 10; Length 628;
Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LRVLLKR 10
Db 224 LRVLLKR 231

```
RESULT 38
US-10-282-122A-49250
; Sequence 49250, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49250
; LENGTH: 789
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49250

Query Match      1.5%; Score 8; DB 15; Length 789;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      324 LNLDPVFG 331
DB      727 LNLDPVFG 734

RESULT 39
US-10-327-598-188
; Sequence 188, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyeppa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: for Making and Using Them
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 194
```

```
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 188
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-188

Query Match      1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      245 GSSATLT 251
DB      12 GSSATLT 18

RESULT 40
US-10-327-598-190
; Sequence 190, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyeppa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: for Making and Using Them
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 190
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-190

Query Match      1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      245 GSSATLT 251
DB      12 GSSATLT 18

RESULT 41
US-10-327-598-194
; Sequence 194, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyeppa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: for Making and Using Them
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 194
```

LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-194

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 42
US-10-327-598-200
Sequence 200, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Honliang
APPLICANT: Aiyappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 200
LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-200

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 43
US-10-327-598-301
Sequence 301, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Honliang
APPLICANT: Aiyappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 301
LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-301

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 44
US-10-327-598-305
Sequence 305, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Honliang
APPLICANT: Aiyappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 305
LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-305

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 45
US-10-327-598-307
Sequence 307, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Honliang
APPLICANT: Aiyappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 307
LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-307

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 245 GSSATLT 251
DB 12 GSSATLT 18

```
RESULT 46
US-10-424-599-184724
; Sequence 184724, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 184724
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_137821C.1.pep
US-10-424-599-184724

Query Match
Best Local Similarity 1.3%; Score 7; DB 15; Length 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 70 SGDIIICL 76
Db 1 SGDIIICL 7

RESULT 47
US-10-424-599-248433
; Sequence 248433, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 248433
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_66365C.1.pep
US-10-424-599-248433

Query Match
Best Local Similarity 1.3%; Score 7; DB 15; Length 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 LRLSLIC 36
Db 29 LRLSLIC 35

RESULT 48
US-10-097-065-226
; Sequence 226, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 60/068, 006
; OTHER INFORMATION: US/10/097, 065

CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 226
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals stop translation
US-10-097-065-226

Query Match
Best Local Similarity 1.3%; Score 7; DB 14; Length 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 323 ALNLPDV 329
Db 43 ALNLPDV 49

RESULT 49
US-10-372-876-226
; Sequence 226, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US/10/372,876
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 09/334,595
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
```

```

; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 226
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals stop translation
US-10-372-876-226
```

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Query Match          1.3%; Score 7; DB 14; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      323 ALNLPDV 329
      |||||
Db      43 ALNLPDV 49
```

```

RESULT 50
US-10-437-963-115025
; Sequence 115025, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 115025
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18660C.1.pep
US-10-437-963-115025
```

```
Query Match          1.3%; Score 7; DB 16; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      508 RPSRGRP 514
      |||||
Db      21 RPSRGRP 27
```

```

RESULT 51
US-10-125-258-76
; Sequence 76, Application US/10125258
; Publication No. US20030028920A1
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
```

```

; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnall, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 76
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-125-258-76
```

```
Query Match          1.3%; Score 7; DB 14; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      352 VLSLSAV 358
      |||||
Db      14 VLSLSAV 20
```

```

RESULT 52
US-10-125-258-77
; Sequence 77, Application US/10125258
; Publication No. US20030028920A1
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnall, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 77
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-125-258-77
```

```
Query Match          1.3%; Score 7; DB 14; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      352 VLSLSAV 358
      |||||
Db      14 VLSLSAV 20
```

```

RESULT 53
US-09-764-891-4887
; Sequence 4887, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
```

;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 10231
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 4887
;; LENGTH: 65
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-764-891-4887

Query Match 1.3%; Score 7; DB 10; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EVPEPTEP 21
|||
56 EVPEPTEP 62

RESULT 54
US-10-424-599-216169
; Sequence 216169, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 216169
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3722C.1.pep
US-10-424-599-216169

Query Match 1.3%; Score 7; DB 15; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 LVYPLLA 318
|||||
52 LVYPLLA 58

RESULT 55
US-10-425-115-280879
; Sequence 280879, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280879
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_19263C.1.pep
US-10-425-115-280879

Query Match 1.3%; Score 7; DB 17; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 PPSSRLP 440
|||||
DB 33 PPSSRLP 39

RESULT 56
US-10-424-599-227458
; Sequence 227458, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 227458
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_47423C.1.pep
US-10-424-599-227458

Query Match 1.3%; Score 7; DB 15; Length 68;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 GDLICLI 77
|||||
DB 52 GDLICLI 58

RESULT 57
US-10-425-115-299912
; Sequence 299912, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 299912
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(69)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_36591C.1.pep
US-10-425-115-299912

Query Match 1.3%; Score 7; DB 17; Length 69;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 137 DSMGPS 143

Db 63 DSMGPS 69

RESULT 58

US-10-437-963-138148
; Sequence 138148, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Bouharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138148
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39563C.1.pep
US-10-437-963-138148

Query Match 1.3%; Score 7; DB 16; Length 72;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 EOPSLAT 108

Db 32 EOPSLAT 38

RESULT 59

US-10-425-115-198221
; Sequence 198221, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 198221
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112356C.1.pep
US-10-425-115-198221

Query Match 1.3%; Score 7; DB 17; Length 72;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 303 KLSRLFK 309

Db 55 KLSRLFK 61

RESULT 60

US-10-767-701-38388
; Sequence 38388, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 38388
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBT-28MAY03-C57312_1.pep
US-10-767-701-38388

Query Match 1.3%; Score 7; DB 16; Length 75;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 DPLTGDE 60

Db 2 DPLTGDE 8

RESULT 61

US-10-424-599-284592
; Sequence 284592, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 284592
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_99011C.1.pep
US-10-424-599-284592

Query Match 1.3%; Score 7; DB 15; Length 76;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 SSTDSH 95

Db 49 SSTDSH 55

RESULT 62

US-10-425-115-192652
; Sequence 192652, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

;; TITLE OF INVENTION: Plants
;; FILE REFERENCE: 38-21(53222)B
;; CURRENT APPLICATION NUMBER: US/10/425,115
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 369326
;; SEQ ID NO 192652
;; LENGTH: 78
;; TYPE: PRT
;; ORGANISM: Zea mays
;; FEATURE:
;; OTHER INFORMATION: Clone ID: MRT4577_107282C.1.pep
US-10-425-115-192652

Query Match 1.3%; Score 7; DB 17; Length 78;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

Qy 105 SLATSSN 111
Db 42 SLATSSN 48

RESULT 63
US-10-425-115-305666
;; Sequence 305666, Application US/10425115
;; Publication No. US20040214272A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants
;; FILE REFERENCE: 38-21(53222)B
;; CURRENT APPLICATION NUMBER: US/10/425,115
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 369326
;; SEQ ID NO 305666
;; LENGTH: 81
;; TYPE: PRT
;; ORGANISM: Zea mays
;; FEATURE:
;; OTHER INFORMATION: Clone ID: MRT4577_41835C.1.pep
US-10-425-115-305666

Query Match 1.3%; Score 7; DB 17; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MRLRVRL 7
Db 10 MRLRVRL 16

RESULT 64
US-10-424-599-167388
;; Sequence 167388, Application US/10424599
;; Publication No. US20040031072A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;; FILE REFERENCE: 38-21(53223)B
;; CURRENT APPLICATION NUMBER: US/10/424,599
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 285684
;; SEQ ID NO 167388
;; LENGTH: 83
;; TYPE: PRT
;; ORGANISM: Glycine max

;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT3847_122169C.1.pep
US-10-424-599-167388

Query Match 1.3%; Score 7; DB 15; Length 83;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

Qy 462 SGLRGP 468
Db 34 SGLRGP 40

RESULT 65
US-10-437-963-200420
;; Sequence 200420, Application US/10437963
;; Publication No. US20040123343A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; APPLICANT: Wu, Wei
;; APPLICANT: Boukhartov, Andrey A.
;; APPLICANT: Bardazuk, Brad
;; APPLICANT: Li, Ping
;; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;; FILE REFERENCE: 38-21(53221)B
;; CURRENT APPLICATION NUMBER: US/10/437,963
;; CURRENT FILING DATE: 2003-05-14
;; NUMBER OF SEQ ID NOS: 204966
;; SEQ ID NO 200420
;; LENGTH: 83
;; TYPE: PRT
;; ORGANISM: Oryza sativa
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT4530_95891C.1.pep
US-10-437-963-200420

Query Match 1.3%; Score 7; DB 16; Length 83;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

Qy 496 PGRGPN 502
Db 11 PGRGPN 17

RESULT 66
US-10-425-115-363121
;; Sequence 363121, Application US/10425115
;; Publication No. US20040214272A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants
;; FILE REFERENCE: 38-21(53222)B
;; CURRENT APPLICATION NUMBER: US/10/425,115
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 369326
;; SEQ ID NO 363121
;; LENGTH: 84
;; TYPE: PRT
;; ORGANISM: Zea mays
;; FEATURE:
;; OTHER INFORMATION: Clone ID: MRT4577_94340C.1.pep
US-10-425-115-363121

Query Match 1.3%; Score 7; DB 17; Length 84;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 NEIRSVK 275
|||||
Db 8 NEIRSVK 14

RESULT 67
US-10-437-963-174548
; Sequence 174548, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174548
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72478C.1.pcp
US-10-437-963-174548

Query Match 1.3%; Score 7; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 RSVLSLS 356
|||||
Db 76 RSVLSLS 82

RESULT 68
US-10-425-115-313746
; Sequence 313746, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 313746
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_49196C.1.pcp
US-10-425-115-313746

Query Match 1.3%; Score 7; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 HURLSL 35
|||||

Db 75 HURLSL 81

RESULT 69
US-09-864-761-38560
; Sequence 38560, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38560
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004217.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.6
; OTHER INFORMATION: SWISSPROT HIT: P47819, EVALUATE 7.40e-01
US-09-864-761-38560

Query Match 1.3%; Score 7; DB 9; Length 89;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 58 GDEETLA 64
DB 42 GDEETLA 48

RESULT 70
US-10-424-599-233924
; Sequence 233924, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovall, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 233924
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(89)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_53258C.1.pcp
US-10-424-599-233924

Query Match 1.3%; Score 7; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 329 VEGLVVL 335
DB 12 VEGLVVL 18

RESULT 71
US-10-437-963-154952
; Sequence 154952, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovall, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 154952
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_54763C.1.pcp
US-10-437-963-154952

Query Match 1.3%; Score 7; DB 16; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 512 GRPTDGR 518
DB 73 GRPTDGR 79

RESULT 72
US-10-029-386-34281
; Sequence 34281, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT FILING DATE: 2001-12-20
; CURRENT APPLICATION NUMBER: US/10/029,386
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34281
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.6
; OTHER INFORMATION: SWISSPROT HIT: P53100, EVALUE 7.60e+00
US-10-029-386-34281

Query Match 1.3%; Score 7; DB 14; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 275 KRLQLLP 281
DB 27 KRLQLLP 33

RESULT 73
US-10-425-115-306931
; Sequence 306931, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovall, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 306931
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_42992C.1.pcp
US-10-425-115-306931

Query Match 1.3%; Score 7; DB 17; Length 92;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 PSLATSS 110
DB 21 PSLATSS 27

```
RESULT 74
US-09-764-860-518
; Sequence 518, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult FALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 518
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-860-518

Query Match      1.3%; Score 7; DB 9; Length 93;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY      217 TEAKALS 223
      |||||
Db      75 TEAKALS 81

RESULT 75
US-10-074-095-518
; Sequence 518, Application US/10074095
; Publication No. US2003007704A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008C1
; CURRENT APPLICATION NUMBER: US/10/074,095
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 09/764,860
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08

; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
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; PRIOR APPLICATION NUMBER: 60/237,039
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; PRIOR APPLICATION NUMBER: 60/237,038
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; PRIOR APPLICATION NUMBER: 60/237,037
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; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
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; PRIOR FILING DATE: 2000-10-20
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; PRIOR FILING DATE: 2000-10-13
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
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PRIOR FILING DATE: 2000-11-08
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/230,438
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PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2000-08-14
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PRIOR APPLICATION NUMBER: 60/249,297
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/232,400
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/231,242
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PRIOR APPLICATION NUMBER: 60/232,399
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,401
PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: 60/241,808
PRIOR FILING DATE: 2000-10-20
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
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PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08

Query Match 1.3%; Score 7; DB 14; Length 93;
Best Local Similarity 100.0%; Pred.No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 75 TEAKALS 81

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Job time : 144 secs

Tue Nov 16 07:54:44 2004

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Page 1

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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:22:05 ; Search time 40 Seconds
(without alignments)

865,450 Million cell updates/sec

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Gapop 60.0 , Capext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	389	74.5	522	4 US-09-591-694-10	Sequence 10, App1
2	330	63.2	443	4 US-09-581-694-8	Sequence 8, App1
3	86	16.5	102	4 US-09-621-976-5935	Sequence 5935, Ap
4	86	16.5	482	4 US-09-385-219A-14	Sequence 14, App1
5	39	7.5	39	4 US-09-385-219A-21	Sequence 21, App1
6	38	7.3	38	3 US-09-172-841-47	Sequence 47, App1
7	38	7.3	38	4 US-08-951-621-47	Sequence 47, App1
8	15	2.9	38	4 US-09-172-841-49	Sequence 49, App1
9	15	2.9	38	4 US-08-951-621-49	Sequence 49, App1
10	8	1.5	304	4 US-09-248-796A-20160	Sequence 20160, A
11	8	1.5	534	4 US-09-270-767-43905	Sequence 43905, A
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13	7	1.3	20	2 US-08-827-618A-38	Sequence 38, App1
14	7	1.3	20	3 US-08-483-952A-38	Sequence 38, App1
15	7	1.3	20	4 US-08-483-952A-38	Sequence 38, App1
16	7	1.3	25	1 US-08-476-501-38	Sequence 38, App1
17	7	1.3	25	1 US-07-792-259-3	Sequence 268, App
18	7	1.3	59	4 US-09-311-021-268	Sequence 268, App
19	7	1.3	63	4 US-09-248-796A-25619	Sequence 25619, A
20	7	1.3	83	4 US-09-513-999C-7211	Sequence 7211, Ap
21	7	1.3	132	2 US-08-647-960-11	Sequence 11, App1
22	7	1.3	136	4 US-09-252-991A-20401	Sequence 20401, A
23	7	1.3	144	4 US-09-252-991A-19404	Sequence 19404, A
24	7	1.3	167	4 US-08-270-767-32101	Sequence 32101, A
25	7	1.3	167	4 US-08-270-767-47338	Sequence 47338, A
26	7	1.3	174	4 US-09-746-801A-43	Sequence 43, App1
27	7	1.3	230	4 US-09-333-809-223	Sequence 223, App
27	7	1.3	230	4 US-09-333-809-228	Sequence 228, App

28	7	1.3	230	4 US-09-746-311B-372	Sequence 372, App
29	7	1.3	230	4 US-09-746-311B-377	Sequence 377, App
30	7	1.3	244	2 US-08-933-750C-23	Sequence 23, App1
31	7	1.3	244	3 US-09-234-613-23	Sequence 23, App1
32	7	1.3	283	4 US-09-270-767-42559	Sequence 42559, A
33	7	1.3	285	4 US-10-101-464A-692	Sequence 692, App
34	7	1.3	290	4 US-09-252-991A-27484	Sequence 27484, A
35	7	1.3	292	4 US-09-724-623-91	Sequence 81, App1
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37	7	1.3	315	4 US-09-326-402C-17	Sequence 17, App1
38	7	1.3	316	2 US-08-647-960-2	Sequence 3, App1
39	7	1.3	316	2 US-08-946-914-15	Sequence 2, App1
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41	7	1.3	316	3 US-08-946-914-17	Sequence 15, App1
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43	7	1.3	316	4 US-09-656-450-15	Sequence 15, App1
44	7	1.3	316	4 US-09-656-450-17	Sequence 17, App1
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47	7	1.3	325	4 US-09-270-767-43002	Sequence 43002, A
48	7	1.3	328	4 US-10-101-464A-534	Sequence 534, App
49	7	1.3	342	2 US-08-483-151-2	Sequence 2, App1
50	7	1.3	343	2 US-08-624-545-1	Sequence 1, App1
51	7	1.3	343	2 US-09-235-716-1	Sequence 1, App1
52	7	1.3	344	3 US-09-024-532-4	Sequence 4, App1
53	7	1.3	344	4 US-09-705-185-4	Sequence 4, App1
54	7	1.3	345	4 US-07-792-259-12	Sequence 12, App1
55	7	1.3	353	3 US-08-997-803-14	Sequence 14, App1
56	7	1.3	363	1 US-08-458-023B-6	Sequence 6, App1
57	7	1.3	364	1 US-07-792-259-17	Sequence 17, App1
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60	7	1.3	386	4 US-10-101-464A-902	Sequence 902, App
61	7	1.3	393	4 US-09-784-077-2	Sequence 2, App1
62	7	1.3	400	4 US-08-845-381E-63	Sequence 63, App1
63	7	1.3	401	3 US-08-289-222E-3	Sequence 3, App1
64	7	1.3	401	3 US-09-054-526B-3	Sequence 3, App1
65	7	1.3	434	4 US-09-516-143A-2	Sequence 2, App1
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68	7	1.3	435	3 US-09-168-406A-7	Sequence 7, App1
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70	7	1.3	468	4 US-09-351-150A-9	Sequence 9, App1
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72	7	1.3	477	4 US-09-134-000C-5553	Sequence 5553, Ap
73	7	1.3	481	4 US-09-252-991A-23317	Sequence 23317, A
74	7	1.3	495	1 US-08-455-559-10	Sequence 10, App1
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76	7	1.3	495	3 PCT-US94-00657-10	Sequence 10, App1
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78	7	1.3	501	4 US-08-981-490B-1	Sequence 1, App1
79	7	1.3	501	4 US-09-386-450D-2	Sequence 2, App1
80	7	1.3	501	4 US-08-930-996A-12	Sequence 12, App1
81	7	1.3	515	3 US-09-134-001C-3565	Sequence 3565, Ap
82	7	1.3	543	3 US-08-161-290-1	Sequence 1, App1
83	7	1.3	584	1 US-08-450-755-1	Sequence 1, App1
84	7	1.3	584	2 US-08-111-907-2	Sequence 2, App1
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86	7	1.3	585	1 US-08-488-718-13	Sequence 13, App1
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88	7	1.3	585	2 US-08-484-530-57	Sequence 57, App1
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91	7	1.3	585	2 US-08-827-618A-57	Sequence 57, App1
92	7	1.3	585	2 US-08-827-618A-59	Sequence 59, App1
93	7	1.3	585	3 US-08-483-952A-57	Sequence 57, App1
94	7	1.3	585	3 US-08-483-952A-59	Sequence 59, App1
95	7	1.3	585	3 US-08-453-040-2	Sequence 2, App1
96	7	1.3	585	3 US-09-043-930-3	Sequence 3, App1
97	7	1.3	585	3 US-09-043-930-4	Sequence 4, App1
98	7	1.3	585	3 US-09-043-930-5	Sequence 5, App1
99	7	1.3	585	3 US-09-043-930-6	Sequence 6, App1
100	7	1.3	585	3 US-09-043-930-7	Sequence 7, App1

ALIGNMENTS

RESULT 1

US-05591-694-10
Sequence 10, Application US/09591694
Patent No. 6638734
GENERAL INFORMATION:
APPLICANT: John C. Reed
APPLICANT: Shu-ichi Matsuzawa
TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
FILE REFERENCE: P-LJ 4220
CURRENT APPLICATION NUMBER: US/09/591,694
CURRENT FILING DATE: 2000-06-09
EARLIER APPLICATION NUMBER: US 09/330,517
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 522
TYPE: PRT
ORGANISM: Homo sapien
US-05591-694-10

Query Match 74.5%; Score 389; DB 4; Length 522;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 489; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	33	SILCTWGYSSNTRETTITLYNDPLTGDEBTLASIGVSDILICILLODDIPAPNIPESST	92
DB	33	SILCTWGYSSNTRETTITLYNDPLTGDEBTLASIGVSDILICILLODDIPAPNIPESST	92
QY	93	SEHSSLQNNQPSLATSSNOTSMODEQPSDSFOGQAQSGVWDDSMLGSSQNFASISQ	152
DB	93	SEHSSLQNNQPSLATSSNOTSMODEQPSDSFOGQAQSGVWDDSMLGSSQNFASISQ	152
QY	153	DNAHMAEGTGYPSBPMKCSSEVGEQVPHSLFTLYGADCSADANDALIVLHLMLESG	212
DB	153	DNAHMAEGTGYPSBPMKCSSEVGEQVPHSLFTLYGADCSADANDALIVLHLMLESG	212
QY	213	IPQGTAKALSMPEKMKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEIR	272
DB	213	IPQGTAKALSMPEKMKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEIR	272
QY	273	SVKRLQILPESFICEKXGENVANTYKDLOKLSLFDQOLVYPLAFTROALNLPDVFGL	332
DB	273	SVKRLQILPESFICEKXGENVANTYKDLOKLSLFDQOLVYPLAFTROALNLPDVFGL	332
QY	333	VVLPLELKLRIFFRLIDVRSVLSAVCRDLFTASNDPLMRFYLIRDFRNTYRVQDTW	392
DB	333	VVLPLELKLRIFFRLIDVRSVLSAVCRDLFTASNDPLMRFYLIRDFRNTYRVQDTW	392
QY	393	KELYRKRIHQKESPKGRFVWLLPSSSTHTTTFYVNPPLHPPFPSSRLPPGIIGGEYQRP	452
DB	393	KELYRKRIHQKESPKGRFVWLLPSSSTHTTTFYVNPPLHPPFPSSRLPPGIIGGEYQRP	452
QY	453	TLFVVGDPISLILGPGSTPSQFPPLRPDPVGPLGPNPILPGRGPNDRPFRPSRS	512
DB	453	TLFVVGDPISLILGPGSTPSQFPPLRPDPVGPLGPNPILPGRGPNDRPFRPSRS	512
QY	513	RPTDGRLSFM 522	
DB	513	RPTDGRLSFM 522	

RESULT 2
US-05591-694-8
Sequence 8, Application US/09591694
Patent No. 6638734
GENERAL INFORMATION:

APPLICANT: John C. Reed
APPLICANT: Shu-ichi Matsuzawa
TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
FILE REFERENCE: P-LJ 4220
CURRENT APPLICATION NUMBER: US/09/591,694
CURRENT FILING DATE: 2000-06-09
EARLIER APPLICATION NUMBER: US 09/330,517
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 443
TYPE: PRT
ORGANISM: Homo sapien
US-05591-694-8

Query Match 63.2%; Score 330; DB 4; Length 443;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	92	DEHSSLQNNQPSLATSSNOTSMODEQPSDSFOGQAQSGVWDDSMLGSSQNFASISQ	151
DB	13	DEHSSLQNNQPSLATSSNOTSMODEQPSDSFOGQAQSGVWDDSMLGSSQNFASISQ	72
QY	152	QNAHMAEGTGYPSBPMKCSSEVGEQVPHSLFTLYGADCSADANDALIVLHLMLESG	211
DB	73	QNAHMAEGTGYPSBPMKCSSEVGEQVPHSLFTLYGADCSADANDALIVLHLMLESG	132
QY	212	YIPQGTAKALSMPEKMKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEI	271
DB	133	YIPQGTAKALSMPEKMKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEI	192
QY	272	RSVKRLQILPESFICEKXGENVANTYKDLOKLSLFDQOLVYPLAFTROALNLPDVFGL	331
DB	193	RSVKRLQILPESFICEKXGENVANTYKDLOKLSLFDQOLVYPLAFTROALNLPDVFGL	252
QY	332	VVLPLELKLRIFFRLIDVRSVLSAVCRDLFTASNDPLMRFYLIRDFRNTYRVQDTW	391
DB	253	VVLPLELKLRIFFRLIDVRSVLSAVCRDLFTASNDPLMRFYLIRDFRNTYRVQDTW	312
QY	392	WELYRKRIHQKESPKGRFVWLLPSSSTHTTTFYVNPPLHPPFPSSRLPPGIIGGEYQRP	451
DB	313	WELYRKRIHQKESPKGRFVWLLPSSSTHTTTFYVNPPLHPPFPSSRLPPGIIGGEYQRP	372
QY	452	PTLFVVGDPISLILGPGSTPSQFPPLRPDPVGPLGPNPILPGRGPNDRPFRPSRS	511
DB	373	PTLFVVGDPISLILGPGSTPSQFPPLRPDPVGPLGPNPILPGRGPNDRPFRPSRS	432
QY	512	GRPTDGRLSFM 522	
DB	433	GRPTDGRLSFM 443	

RESULT 3
US-05591-694-5935
Sequence 5935, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Mline Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5935
LENGTH: 102
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

Tue Nov 16 07:54:44 2004

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Page 3

NAME/KEY: UNSURE
LOCATION: 87
OTHER INFORMATION: Xaa = Cys, Gly
US-09-621-976-5935

Query Match 16.5%; Score 86; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 5.2e-78;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 413 MLPPSSHTTTPFNPPLHPPPPSSRLPPGIIIGEDDRTLLPYVGDPISSLIPGGETP 472
DB 1 MLPPSSHTTTPFYNPLHPPPPSSRLPPGIIIGEDDRTLLPYVGDPISSLIPGGETP 60

QY 473 SCFPPPLRPDPVGPLGPNPILPGR 498
DB 61 SCFPPPLRPDPVGPLGPNPILPGR 86

RESULT 4
US-09-385-219A-14
Sequence 14, Application US/09385219A
Patent No. 6720181
GENERAL INFORMATION:
APPLICANT: Chateau, D.
APPLICANT: Pagano, M.
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
FILE REFERENCE: 5914-081
CURRENT APPLICATION NUMBER: US/09/385,219A
CURRENT FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/058,355
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 60/118,568
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: 60/124,449
PRIOR FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 482
TYPE: PRT
ORGANISM: Homo sapiens
US-09-385-219A-14

Query Match 16.5%; Score 86; DB 4; Length 482;
Best Local Similarity 100.0%; Pred. No. 2.2e-77;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LCEGSSATLTCVPLGNLIYVNAATKINNEIRSVKRLQDLDPESFICKKIGENVANYKDL 301
DB 202 LCEGSSATLTCVPLGNLIYVNAATKINNEIRSVKRLQDLDPESFICKKIGENVANYKDL 261
QY 302 QKLSRLFKDQVYPLLAFTQALNLP 327
DB 262 QKLSRLFKDQVYPLLAFTQALNLP 287

RESULT 5
US-09-385-219A-21
Sequence 21, Application US/09385219A
Patent No. 6720181
GENERAL INFORMATION:
APPLICANT: Chateau, D.
APPLICANT: Pagano, M.
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
FILE REFERENCE: 5914-081
CURRENT APPLICATION NUMBER: US/09/385,219A
CURRENT FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/098,355
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 60/118,568
PRIOR FILING DATE: 1999-02-03

PRIOR APPLICATION NUMBER: 60/124,449
PRIOR FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
US-09-385-219A-21

Query Match 7.5%; Score 39; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.4e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLELKLRIFFRLDVRSVLSAVCRDLFTASNDPLMW 373
DB 1 LPLELKLRIFFRLDVRSVLSAVCRDLFTASNDPLMW 39

RESULT 6
US-09-172-841-47
Sequence 47, Application US/09172841
Patent No. 6232081
GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Elledge, Stephen J.
TITLE OF INVENTION: F-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/172,841
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 47
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-172-841-47

Query Match 7.3%; Score 38; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.3e-30;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLELKLRIFFRLDVRSVLSAVCRDLFTASNDPLMW 372
DB 1 LPLELKLRIFFRLDVRSVLSAVCRDLFTASNDPLMW 38

RESULT 7
US-08-951-621-47
Sequence 47, Application US/08951621
Patent No. 6573094
GENERAL INFORMATION:
APPLICANT: HARPER, JEFFREY W.
APPLICANT: ELLEDGE, STEPHEN J.
TITLE OF INVENTION: F-BOX GENES AND PROTEINS
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,621
FILING DATE: 16-OCT-1997

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: BCM-02999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-951-621-47

Query Match
Best Local Similarity 100.0%; Score 38; DB 4; Length 38;
Pred. No. 2.3e-30;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLELKLRIFFRLDVSLSAVCRDIFTSNDPLIM 372
Db 1 LPLELKLRIFFRLDVSLSAVCRDIFTSNDPLIM 38

RESULT 8
US-09-172-841-49
Sequence 49, Application US/09172841
Patent No. 6232081
GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Elledge, Stephen J.
TITLE OF INVENTION: F-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/172,841
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 49
LENGTH: 38
TYPE: PRT
ORGANISM: Mus musculus
US-09-172-841-49

Query Match
Best Local Similarity 100.0%; Score 15; DB 3; Length 38;
Pred. No. 2.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLELKLRIFFRLDV 349
Db 1 LPLELKLRIFFRLDV 15

RESULT 9
US-08-951-621-49
Sequence 49, Application US/08951621
Patent No. 6573094
GENERAL INFORMATION:
APPLICANT: HARPER, JEFFREY W.
APPLICANT: ELLEDGE, STEPHEN J.
TITLE OF INVENTION: F-BOX GENES AND PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,621
FILING DATE: 16-OCT-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: BCM-02999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-951-621-49

Query Match
Best Local Similarity 100.0%; Score 15; DB 4; Length 38;
Pred. No. 2.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLELKLRIFFRLDV 349
Db 1 LPLELKLRIFFRLDV 15

RESULT 10
US-09-248-796A-20160
Sequence 20160, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20160
LENGTH: 304
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20160

Query Match
Best Local Similarity 1.5%; Score 8; DB 4; Length 304;
Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 LVVLPLEL 339
Db 22 LVVLPLEL 29

RESULT 11
US-09-270-767-43905
Sequence 43905, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43905
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43905

Query Match 1.5%; Score 8; DB 4; Length 534;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 TRFTITLN 51
Db 98 TRFTITLN 105

RESULT 12
US-08-484-530-38
; Sequence 38, Application US/08484530
; Patent No. 5846740
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J
; APPLICANT: Erlander, Mark G
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,530
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Treacartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-530-38

Query Match 1.3%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWKLSGV 233
Db 9 KWKLSGV 15

RESULT 13
US-08-827-618A-38

; Sequence 38, Application US/08827618A
; Patent No. 5998366
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J
; APPLICANT: Erlander, Mark G
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,618A
; FILING DATE: 09-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,725
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/716,909
; FILING DATE: 18-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/586,536
; FILING DATE: 21-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Treacartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-618A-38

Query Match 1.3%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWKLSGV 233
Db 9 KWKLSGV 15

RESULT 14
US-08-483-952A-38
; Sequence 38, Application US/08483952A
; Patent No. 6011139
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J
; APPLICANT: Erlander, Mark G
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA

COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,859
FILING DATE: 17-SEP-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Treccarlin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-952A-38

Query Match 1.3%; Score 7; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWKLSGV 233
|||
9 KWKLSGV 15

RESULT 15
US-08-476-501-38
Sequence 38, Application US/08476501
Patent No. 6455267
GENERAL INFORMATION:
APPLICANT: TOBIN, Allan J.
APPLICANT: ERLANDER, Mark G.
APPLICANT: KAUFMAN, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Teat, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,501
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertam I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A60780-10/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-501-38

Query Match 1.3%; Score 7; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWKLSGV 233
|||
9 KWKLSGV 15

RESULT 16
US-07-792-259-3
Sequence 3, Application US/07792259
Patent No. 5286638
GENERAL INFORMATION:
APPLICANT: TANAKA, YOSHIKAZU
APPLICANT: ASHIVARI, TOSHIHIKO
APPLICANT: HATANAKA, HARUO
APPLICANT: SHIBANO, YUJI
APPLICANT: AMACHI, TERUO
APPLICANT: NAKAYAMA, TORU
APPLICANT: SUMIDA, MOTOO
TITLE OF INVENTION: PEROXIDE GENE OF MICROBIAL ORIGIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L. STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,259
FILING DATE: 19911115
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 9437/93433
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-792-259-3

Query Match 1.3%; Score 7; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPGPG 469
|||||
DB 10 SLIPGPG 16

RESULT 17

US-09-311-021-268
; Sequence 268, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 268
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-311-021-268

Query Match 1.3%; Score 7; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 PGPGETP 472
|||||
DB 27 PGPGETP 33

RESULT 18
US-09-248-796A-25619
; Sequence 25619, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25619
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-25619

Query Match 1.3%; Score 7; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 ICLILDD 80
|||||
DB 19 ICLILDD 25

RESULT 19
US-09-513-999C-7211

; Sequence 7211, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, G.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7211
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens

; NAME/KEY: UNSURE
; LOCATION: 12
; OTHER INFORMATION: Xaa=Arg or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 29
; OTHER INFORMATION: Xaa=Arg or Ser
US-09-513-999C-7211

Query Match 1.3%; Score 7; DB 4; Length 83;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 KRLQILP 281
|||||
DB 21 KRLQILP 27

RESULT 20
US-08-647-960-11
; Sequence 11, Application US/08647960
; Patent No. 5908761
; GENERAL INFORMATION:
; APPLICANT: ZICK, Yehiel
; TITLE OF INVENTION: GALECTIN-8 AND GALECTIN-8-LIKE PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,960
; FILING DATE: 30-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107880
; FILING DATE: 05-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: ZICK=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3527
; INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 132 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-647-960-11

Query Match 1.3%; Score 7; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 345 RLDDRS 351
 DB 125 RLDDRS 131

RESULT 21
 US-09-252-991A-20401
 ; Sequence 20401, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 20401
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-20401

Query Match 1.3%; Score 7; DB 4; Length 136;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 IPQTEA 219
 DB 79 IPQTEA 85

RESULT 22
 US-09-252-991A-19404
 ; Sequence 19404, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 19404
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-19404

Query Match 1.3%; Score 7; DB 4; Length 144;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 TSSNOTS 114
 DB 130 TSSNOTS 136

RESULT 23
 US-09-270-767-32121
 ; Sequence 32121, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 32121
 ; LENGTH: 167
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-270-767-32121

Query Match 1.3%; Score 7; DB 4; Length 167;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 PGETPSQ 474
 DB 48 PGETPSQ 54

RESULT 24
 US-09-270-767-47338
 ; Sequence 47338, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 47338
 ; LENGTH: 167
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-270-767-47338

Query Match 1.3%; Score 7; DB 4; Length 167;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 PGETPSQ 474
 DB 48 PGETPSQ 54

RESULT 25
 US-09-746-801A-43
 ; Sequence 43, Application US/09746801A
 ; Patent No. 6689940
 ; GENERAL INFORMATION:
 ; APPLICANT: Wagner, et al.
 ; TITLE OF INVENTION: GENES REGULATING CIRCADIAN CLOCK FUNCTION AND PHOTOPERIODISM
 ; FILE REFERENCE: 1505-54357
 ; CURRENT APPLICATION NUMBER: US/09/746,801A
 ; CURRENT FILING DATE: 2000-12-20
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 43

LENGTH: 174
; TYPE: PRT
; ORGANISM: Pismum sativum
US-09-746-801A-43

Query Match 1.3%; Score 7; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 VPHSLER 185
Db 159 VPHSLER 165

RESULT 26
US-09-333-809-223
; Sequence 223, Application US/09333809
; Patent No. 6667175
; GENERAL INFORMATION:
; APPLICANT: Suciu-Foca, Nicole
; TITLE OF INVENTION: GENERATION OF ANTIGEN SPECIFIC T SUPPRESSOR CELLS FOR TREATMENT
; FILE REFERENCE: 0575/58332
; CURRENT APPLICATION NUMBER: US/09/333,809
; CURRENT FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 223
; LENGTH: 230
; TYPE: PRT
; ORGANISM: swine
US-09-333-809-223

Query Match 1.3%; Score 7; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 EHSSLON 100
Db 177 EHSSLON 183

RESULT 27
US-09-333-809-228
; Sequence 228, Application US/09333809
; Patent No. 6667175
; GENERAL INFORMATION:
; APPLICANT: Suciu-Foca, Nicole
; TITLE OF INVENTION: GENERATION OF ANTIGEN SPECIFIC T SUPPRESSOR CELLS FOR TREATMENT
; FILE REFERENCE: 0575/58332
; CURRENT APPLICATION NUMBER: US/09/333,809
; CURRENT FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
; LENGTH: 230
; TYPE: PRT
; ORGANISM: swine
US-09-333-809-228

Query Match 1.3%; Score 7; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 EHSSLON 100
Db 177 EHSSLON 183

RESULT 28
US-09-746-311B-372
; Sequence 372, Application US/09746311B

Patent No. 6759239
; GENERAL INFORMATION:
; APPLICANT: Suciu-Foca, Nicole
; APPLICANT: Liu, Zhuro
; APPLICANT: Chang, Chih-Chao
; APPLICANT: Cortesini, Raffaello
; TITLE OF INVENTION: Generation of Antigen-Specific T Suppressor Cells For Treatment of
; FILE REFERENCE: 0575/58332-B
; CURRENT APPLICATION NUMBER: US/09/746,311B
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US00/16594
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 382
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 372
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Swine SLA-DOB
US-09-746-311B-372

Query Match 1.3%; Score 7; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 EHSSLON 100
Db 177 EHSSLON 183

RESULT 29
US-09-746-311B-377
; Sequence 377, Application US/09746311B
; Patent No. 6759239
; GENERAL INFORMATION:
; APPLICANT: Suciu-Foca, Nicole
; APPLICANT: Liu, Zhuro
; APPLICANT: Chang, Chih-Chao
; APPLICANT: Cortesini, Raffaello
; TITLE OF INVENTION: Generation of Antigen-Specific T Suppressor Cells For Treatment of
; FILE REFERENCE: 0575/58332-B
; CURRENT APPLICATION NUMBER: US/09/746,311B
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US00/16594
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 382
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 377
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Swine SLA-DOB
US-09-746-311B-377

Query Match 1.3%; Score 7; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 EHSSLON 100
Db 177 EHSSLON 183

RESULT 30
US-08-933-750C-23
; Sequence 23, Application US/08933750C
; Patent No. 5932442
; GENERAL INFORMATION:
; APPLICANT: Lai, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Tanice

APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLNOT04
CLONE: 1561587
US-08-933-750C-23

Query Match 1.3%; Score 7; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 DVSYS 354
DB 229 DVSYS 235

RESULT 31
US-09-234-613-23
Sequence 23, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Tai, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLNOT04
CLONE: 1561587
US-09-234-613-23

Query Match 1.3%; Score 7; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 DVSYS 354
DB 229 DVSYS 235

RESULT 32
US-09-270-767-42559
Sequence 42559, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-034
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42559
LENGTH: 283
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-42559

Query Match 1.3%; Score 7; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 DVSYS 354
DB 268 DVSYS 274

RESULT 33
US-10-101-464A-692
Sequence 692, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:


```

; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 682
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-692

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```

Query Match          1.3%; Score 7; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      351 SVLSLSA 357
        |||||
Db      88 SVLSLSA 94

```

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RESULT 34
US-09-252-991A-27484
; Sequence 27484, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 27484
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27484

```

```

Query Match          1.3%; Score 7; DB 4; Length 290;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      466 PGPGETP 472
        |||||
Db      277 PGPGETP 283

```

```

RESULT 35
US-09-724-623-81
; Sequence 81, Application US/09724623
; Patent No. 6476209
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Lubbers, Mark W
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides, materials incorporating

```

```

; TITLE OF INVENTION: them, and methods for using them.
; FILE REFERENCE: 1048U1
; CURRENT APPLICATION NUMBER: US/09/724,623
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 81
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-724-623-81

```

```

Query Match          1.3%; Score 7; DB 4; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      312 LVYPILA 318
        |||||
Db      141 LVYPILA 147

```

```

RESULT 36
US-09-252-991A-25548
; Sequence 25548, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 25548
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25548

```

```

Query Match          1.3%; Score 7; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      104 PSLATSS 110
        |||||
Db      32 PSLATSS 38

```

```

RESULT 37
US-09-326-402C-17
; Sequence 17, Application US/09326402C
; Patent No. 6759192
; GENERAL INFORMATION:
; APPLICANT: Bougenfelder, Marta
; APPLICANT: Bougenfelder, Lydia
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (PCTA-1)
; FILE REFERENCE: GEN-7112X01
; CURRENT APPLICATION NUMBER: US/09/326,402C
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,187
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/102,324
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 17
; LENGTH: 315
; TYPE: PRT

```

ORGANISM: Mus musculus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1) (315)
OTHER INFORMATION: amino acid sequence of PCTA.mus
US-09-326-402C-17

Query Match 1.3%; Score 7; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 345 RLLDVS 351
Db 308 RLLDVS 314

RESULT 38
US-08-728-521-3
Sequence 3, Application US/08728521
Patent No. 5869289
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: HUMAN GALECTIN HOMOLOG
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,521
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0137 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 717032
US-08-728-521-3

Query Match 1.3%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 345 RLLDVS 351
Db 309 RLLDVS 315

RESULT 39
US-08-647-960-2

Sequence 2, Application US/08647960
Patent No. 5908761
GENERAL INFORMATION:
APPLICANT: Zick, Yehiel
TITLE OF INVENTION: GALECTIN-8 AND GALECTIN-8-LIKE PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NETWORK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,960
FILING DATE: 30-MAY-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107880
FILING DATE: 05-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: ZICK=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3527
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-647-960-2

Query Match 1.3%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 345 RLLDVS 351
Db 309 RLLDVS 315

RESULT 40
US-08-946-914-15
Sequence 15, Application US/08946914
Patent No. 6027916
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,914

FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-946-914-15

Query Match 1.3%; Score 7; DB 3; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 RLLDVS 351
Db 309 RLLDVS 315

RESULT 41
US-08-946-914-17
Sequence 17, Application US/08946914
Patent No. 6027916
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Galectin 8, 9, 10 and 10sv
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,914
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein

US-08-946-914-17

Query Match 1.3%; Score 7; DB 3; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 RLLDVS 351
Db 309 RLLDVS 315

RESULT 42
US-09-212-146-3
Sequence 3, Application US/09212146
Patent No. 6281333
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: HUMAN GALECTIN HOMOLOG
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/212,146
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/728,521
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0137 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 717032
US-09-212-146-3

Query Match 1.3%; Score 7; DB 3; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 RLLDVS 351
Db 309 RLLDVS 315

RESULT 43
US-09-656-450-15
Sequence 15, Application US/09656450
Patent No. 6468768
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.

```

; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides
; FILE REFERENCE: 1488.0560003
; CURRENT APPLICATION NUMBER: US/09/656,450
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/263,689
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 08/946,914
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: US 60/028,093
; PRIOR FILING DATE: 1996-10-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Rat
; US-09-656-450-15

Query Match      1.3%; Score 7; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      345 RLDDVS 351
      |||||
      |||||
Db      309 RLDDVS 315

RESULT 44
US-09-656-450-17
; Sequence 17, Application US/09656450
; Patent No. 6468768
; GENERAL INFORMATION:
; APPLICANT: Gentz, Retner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides
; FILE REFERENCE: 1488.0560003
; CURRENT APPLICATION NUMBER: US/09/656,450
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/263,689
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 08/946,914
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: US 60/028,093
; PRIOR FILING DATE: 1996-10-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Rat
; US-09-656-450-17

Query Match      1.3%; Score 7; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      345 RLDDVS 351
      |||||
      |||||
Db      309 RLDDVS 315

RESULT 45
US-09-326-402C-9
; Sequence 9, Application US/09326402C
; Patent No. 6759192
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougeneloret, Lydie
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (POTA-1
; FILE REFERENCE: GEN-7112XCI
```

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; CURRENT APPLICATION NUMBER: US/09/326,402C
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/086,187
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/102,324
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-326-402C-9

Query Match      1.3%; Score 7; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      345 RLDDVS 351
      |||||
      |||||
Db      309 RLDDVS 315

RESULT 46
US-09-252-991A-20523
; Sequence 20523, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20523
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-20523

Query Match      1.3%; Score 7; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLVRRL 8
      |||||
      |||||
Db      54 RLVRRL 60

RESULT 47
US-09-270-767-43002
; Sequence 43002, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43002
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-43002
```

Query Match 1.3%; Score 7; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 VLPELTK 340
DB 108 VLPELTK 114

RESULT 48
US-10-101-464A-534
Sequence 534, Application US/10101464A
Patent No. 6768841
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020C2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 534
LENGTH: 328
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-10-101-464A-534

Query Match 1.3%; Score 7; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 DEETLAS 65
DB 216 DEETLAS 222

RESULT 49
US-08-483-151-2
Sequence 2, Application US/08483151
Patent No. 5858752
GENERAL INFORMATION:
APPLICANT: Seed, Brian
TITLE OF INVENTION: FUCOSYLTRANSFERASE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,151
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/278001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-151-2

Query Match 1.3%; Score 7; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRVRL 8
DB 304 RLRVRL 310

RESULT 50
US-08-624-545-1
Sequence 1, Application US/08624545
Patent No. 5817495
GENERAL INFORMATION:
APPLICANT: Pedersen, Anders
APPLICANT: Vind, Jesper
APPLICANT: Svendsen, Allan
APPLICANT: Cherry, Joel
APPLICANT: Lamsa, Michael
APPLICANT: Schneider, Paule
TITLE OF INVENTION: H2O2-Stable Peroxidase Variants
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58174950 No. 58174950th America
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,545
FILING DATE: 07-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 4072.204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-624-545-1

Query Match 1.3%; Score 7; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
 |||||
 DB 150 SLIPPG 156

RESULT 51

US-09-235-736-1
 ; Sequence 1, Application US/09235736
 ; Patent No. 5968883
 ; GENERAL INFORMATION:
 ; APPLICANT: Cherry, Joel
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Damus, Ture
 ; APPLICANT: Schneider, Palle
 ; TITLE OF INVENTION: Peroxidase Variants
 ; FILE REFERENCE: 4938.204-US
 ; CURRENT APPLICATION NUMBER: US/09/235,736
 ; CURRENT FILING DATE: 1999-01-22
 ; EARLIER APPLICATION NUMBER: 0937/96
 ; EARLIER FILING DATE: 1996-09-03
 ; EARLIER APPLICATION NUMBER: PCT/DK97/00361
 ; EARLIER FILING DATE: 1997-09-02
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 343
 ; TYPE: PRT
 ; ORGANISM: Coprinus cinereus
 ; US-09-235-736-1

Query Match 1.3%; Score 7; DB 2; Length 343;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
 |||||
 DB 150 SLIPPG 156

RESULT 52

US-09-024-532-4
 ; Sequence 4, Application US/09024532
 ; Patent No. 6245901
 ; GENERAL INFORMATION:
 ; APPLICANT: von der Osten, Claus
 ; APPLICANT: Olsen, Arne Agerlin
 ; APPLICANT: Røsgen, Erwin Ludo
 ; TITLE OF INVENTION: A Modified Polypeptide
 ; FILE REFERENCE: 4923.204-US
 ; CURRENT APPLICATION NUMBER: US/09/024,532
 ; CURRENT FILING DATE: 1998-02-17
 ; EARLIER APPLICATION NUMBER: PCT/DK98/00046
 ; EARLIER FILING DATE: 1998-02-06
 ; EARLIER APPLICATION NUMBER: 0135/97
 ; EARLIER FILING DATE: 1997-02-06
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: Arthromyces ramosus
 ; US-09-024-532-4

Query Match 1.3%; Score 7; DB 3; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
 |||||
 DB 151 SLIPPG 157

RESULT 53

US-09-705-185-4
 ; Sequence 4, Application US/09705185
 ; Patent No. 6623950
 ; GENERAL INFORMATION:
 ; APPLICANT: von der Osten, Claus
 ; APPLICANT: Olsen, Arne Agerlin
 ; APPLICANT: Røsgen, Erwin Ludo
 ; TITLE OF INVENTION: A Modified Polypeptide
 ; FILE REFERENCE: 4923.204-US
 ; CURRENT APPLICATION NUMBER: US/09/705,185
 ; CURRENT FILING DATE: 2000-11-02
 ; PRIOR APPLICATION NUMBER: 09/024,532
 ; PRIOR FILING DATE: 1998-02-17
 ; PRIOR APPLICATION NUMBER: PCT/DK98/00046
 ; PRIOR FILING DATE: 1998-02-06
 ; PRIOR APPLICATION NUMBER: 0135/97
 ; PRIOR FILING DATE: 1997-02-06
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: Arthromyces ramosus
 ; US-09-705-185-4

Query Match 1.3%; Score 7; DB 4; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
 |||||
 DB 151 SLIPPG 157

RESULT 54

US-07-792-259-12
 ; Sequence 12, Application US/07792259
 ; Patent No. 5286638
 ; GENERAL INFORMATION:
 ; APPLICANT: TANAKA, YOSHIKAZU
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; APPLICANT: HATANAKA, HARUO
 ; APPLICANT: SHIBANO, YUJI
 ; APPLICANT: AMACHI, TERUO
 ; APPLICANT: NAKAYAMA, TORU
 ; APPLICANT: SUMIDA, MOTOO
 ; TITLE OF INVENTION: PEROXIDE GENE OF MICROBIAL ORIGIN
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
 ; STREET: 1615 L. STREET, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC Compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/792,259
 ; FILING DATE: 19911115
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SCOTT, WATSON T.
 ; REGISTRATION NUMBER: 26581
 ; REFERENCE/DOCKET NUMBER: 9437/93433
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3067
 ; TELEFAX: 202-822-0944

TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-792-259-12

Query Match 1.3%; Score 7; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
Db 152 SLIPPG 158

RESULT 55
US-08-997-803-14
Sequence 14, Application US/08997803
Patent No. 6057126
GENERAL INFORMATION:
APPLICANT: CHUN, Jerold J. M.
APPLICANT: GUPPA, Ashwani
APPLICANT: MUNROE, Donald G.
APPLICANT: VYAS, Tejal B.
TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mikaido, Martelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street, N.W., Suite 330
City: Washington
STATE: D. C.
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,803
FILING DATE: 24-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wong, King L.
REGISTRATION NUMBER: 37,500
REFERENCE/DOCKET NUMBER: P8074-7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-803-14

Query Match 1.3%; Score 7; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 GLVVLPL 337
Db 255 GLVVLPL 261

RESULT 56
US-08-458-023B-6
Sequence 6, Application US/08458023B

Patent No. 5667990
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boomathnan, Karuppan C.
TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56679900 No. 5667990disk of No. 5667990th America, Inc.
STREET: 405 Lexington Avenue
City: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowmey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-8655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-023B-6

Query Match 1.3%; Score 7; DB 1; Length 363;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
Db 170 SLIPPG 176

RESULT 57
US-07-792-259-17
Sequence 17, Application US/07792259
Patent No. 5286638
GENERAL INFORMATION:
APPLICANT: TANAKA, YOSHIKAZU
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: HATANAKA, HARUYO
APPLICANT: SHIBANO, YUJI
APPLICANT: AWACHI, TERUO
APPLICANT: NAKAYAMA, TORU
APPLICANT: SUMIDA, MOTOO
TITLE OF INVENTION: PEROXIDE GENE OF MICROBIAL ORIGIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L. STREET, N.W.
City: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,259
FILING DATE: 1991.11.5
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 9437/93433
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-792-259-17

Query Match 1.3%; Score 7; DB 1; Length 364;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
DB 171 SLIPPG 177

RESULT 58
US-09-270-767-39038
Sequence 39038, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39038
LENGTH: 383
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-39038

Query Match 1.3%; Score 7; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRSHRL 32
DB 13 LRSHRL 19

RESULT 59
US-09-270-767-54255
Sequence 54255, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54255

LENGTH: 383
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-54255

Query Match 1.3%; Score 7; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRSHRL 32
DB 13 LRSHRL 19

RESULT 60
US-10-101-464A-902
Sequence 902, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions isolated from plant cells
TITLE OF INVENTION: and their use in the modification of plant cell signaling
FILE REFERENCE: 11000.1020c2
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: Pasteo for Windows Version 4.0
SEQ ID NO 902
LENGTH: 386
TYPE: PRT
ORGANISM: Pinus radiata
US-10-101-464A-902

Query Match 1.3%; Score 7; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 SVLSLSA 357
DB 277 SVLSLSA 283

RESULT 61
US-09-784-077-2
Sequence 2, Application US/09784077
Patent No. 6693183
GENERAL INFORMATION:
APPLICANT: NATSUKA, SHUNJI
APPLICANT: GERSTEN, KEVIN M.
TITLE OF INVENTION: MURINE ALPHA (1,3) FUCOSYLTRANSFERASE
FUC-TVII, DNA ENCODING THE SAME, METHOD FOR PREPARING THE
SAME, ANTIBODIES RECOGNIZING THE SAME, IMMUNOASSAYS FOR
DETECTING THE SAME, PLASMIDS CONTAINING SUCH DNA
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA

COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,077
FILING DATE: 16-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/613,098
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: LAVALLEYE, JEAN-PAUL
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-114-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-784-077-2

Query Match 1.3%; Score 7; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRYRL 8
Db 355 RLRYRL 361

RESULT 62
US-08-845-381E-63
Sequence 63, Application US/08845381E
Patent No. 6602681
GENERAL INFORMATION:
APPLICANT: OHSHYE, Kazuhiro
APPLICANT: KITANO, Katsuhiko
APPLICANT: TANAKA, Sho-ji
APPLICANT: MATSUO, Hisayuki
APPLICANT: MIZUNO, Kensaku
TITLE OF INVENTION: RECOMBINANT C-TERMINAL ALPHA-AMIDATING
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DONALD, SWECKER & MATTHEWS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,381E
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 621778184
FILING DATE: 17-JUL-1987
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 62306867
FILING DATE: 05-DEC-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/219,375
FILING DATE: 15-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/509,583
FILING DATE: 16-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 001560-296
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
US-08-845-381E-63

Query Match 1.3%; Score 7; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 NIPSTD 92
Db 111 NIPSTD 117

RESULT 63
US-08-289-222E-3
Sequence 3, Application US/08289222E
Patent No. 6120760
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARKELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222E
FILING DATE: 25-AUG-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350

FILED DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-222B-3

Query Match 1.3%; Score 7; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
DB 177 LLDVRSV 183

RESULT 64
US-09-054-526B-3
Sequence 3, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: H. TITEN, GERTTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: BOHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAI DO, MARWELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-526B-3

Query Match 1.3%; Score 7; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
DB 177 LLDVRSV 183

RESULT 65
US-09-516-143A-2
Sequence 2, Application US/09516143A
Patent No. 6333182
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Glycosylation Enzymes
FILE REFERENCE: P505BCT
CURRENT APPLICATION NUMBER: US/09/516,143A
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/122,409
PRIOR FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 434
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: 133
OTHER INFORMATION: Xaa equals Tyr or His
NAME/KEY: SITE
LOCATION: 136
OTHER INFORMATION: Xaa equals Gly or Val
NAME/KEY: SITE
LOCATION: 147
OTHER INFORMATION: Xaa equals Ser or Pro
NAME/KEY: SITE
LOCATION: 169
OTHER INFORMATION: Xaa equals Gly or Val
US-09-516-143A-2

Query Match 1.3%; Score 7; DB 3; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 RPSGRP 514
DB 18 RPSGRP 24

RESULT 66
US-09-984-205-2
Sequence 2, Application US/09984205
Patent No. 6783971
GENERAL INFORMATION:
APPLICANT: Coleman, Timothy A. et al.
TITLE OF INVENTION: Human Glycosylation Enzymes
FILE REFERENCE: P505D1
CURRENT APPLICATION NUMBER: US/09/984,205
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: PCT/US00/05325
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/516,143

PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/122,409
PRIOR FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 434
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: 133
OTHER INFORMATION: Xaa equals Tyr or His
NAME/KEY: SITE
LOCATION: 136
OTHER INFORMATION: Xaa equals Gly or Val
NAME/KEY: SITE
LOCATION: 147
OTHER INFORMATION: Xaa equals Ser or Pro
NAME/KEY: SITE
LOCATION: 169
OTHER INFORMATION: Xaa equals Gly or Val
US-09-984-205-2

Query Match 1.3%; Score 7; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 RPSRGP 514
Db 18 RPSRGP 24

RESULT 67
US-08-331-515A-2
Sequence 2, Application US/08331515A
Patent No. 5851811
GENERAL INFORMATION:
APPLICANT: Wellinder, Karen
TITLE OF INVENTION: PEROXIDASE VARIANTS WITH IMPROVED
TITLE OF INVENTION: HYDROGEN PEROXIDE STABILITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5851811 No. 5851811disk of No. 5851811th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,515A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3769,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
STRADEDNESS: single
TOPOLOGY: linear
US-08-331-515A-2

Query Match 1.3%; Score 7; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPGP 469
Db 171 SLIPGP 177

RESULT 68
US-09-168-406A-2
Sequence 2, Application US/09168406A
Patent No. 6258769
GENERAL INFORMATION:
APPLICANT: Wellinder, Karen G.
TITLE OF INVENTION: Peroxidase Variants With Improved
TITLE OF INVENTION: Hydrogen Peroxidase Stability
FILE REFERENCE: 3769,214-US
CURRENT APPLICATION NUMBER: US/09/168,406A
CURRENT FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 08/331,515
PRIOR FILING DATE: 1994-11-01
PRIOR APPLICATION NUMBER: PCT/DP93/00189
PRIOR FILING DATE: 1993-06-01
PRIOR APPLICATION NUMBER: 0792/92
PRIOR FILING DATE: 1992-06-01
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 435
TYPE: PRT
ORGANISM: Coprinus cinereus
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(435)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-168-406A-2

Query Match 1.3%; Score 7; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPGP 469
Db 171 SLIPGP 177

RESULT 69
US-09-198-452A-7
Sequence 7, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevent
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 7
LENGTH: 460
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-7

Query Match 1.3%; Score 7; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 LOCKSRL 307

Db 292 LOKLSRL 298

RESULT 70
US-09-351-150A-9
; Sequence 9, Application US/09351150A
; Patent No. 653817
; GENERAL INFORMATION:
; APPLICANT: Davick, J
; TITLE OF INVENTION: Compositions and Methods for Fumonisin Detoxification
; FILE REFERENCE: 035718/167616, 5718-62
; CURRENT APPLICATION NUMBER: US/09/351,150A
; CURRENT FILING DATE: 1998-07-12
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Bacterium 2412.1
US-09-351-150A-9

Query Match 1.3%; Score 7; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 NDALIVL 202
Db 246 NDALIVL 252

RESULT 71
US-09-252-991A-24392
; Sequence 24392, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24392
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24392

Query Match 1.3%; Score 7; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 GDEETLA 64
Db 448 GDEETLA 454

RESULT 72
US-09-252-991A-27516
; Sequence 27516, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27516
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27516

Query Match 1.3%; Score 7; DB 4; Length 477;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 LYLRDFR 381
Db 233 LYLRDFR 239

RESULT 73
US-09-134-000C-5553
; Sequence 5553, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5553
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5553

Query Match 1.3%; Score 7; DB 4; Length 477;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 TLVQSAD 191
Db 33 TLVQSAD 39

RESULT 74
US-09-252-991A-23317
; Sequence 23317, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23317
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23317

Query Match 1.3%; Score 7; DB 4; Length 481;

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Page 23

Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 RPSRGRP 514
Db 145 RPSRGRP 151

RESULT 75
US-08-455-559-10
; Sequence 10, Application US/08455559
; Patent No. 5801014
; GENERAL INFORMATION:
; APPLICANT: LEE, SE-JIN
; APPLICANT: HUYNH, THANH
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,559
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/003,144
; FILING DATE: 12-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. PH.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD2280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-455-559-10

Query March 1.3%; Score 7; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
Db 271 LLDVRSV 277

Search completed: November 16, 2004, 07:31:38
Job time : 43 secs

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